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| <b>(54) Title:</b> HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW<br><br><b>(57) Abstract</b><br><p>This invention provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of: (a) a sequence selected from SEQ ID Nos 1 to 1193 from the attached sequence listings; (b) an allelic variation of a sequence as defined in (a); or (c) a sequence complementary to (a) or (b). The invention includes uses of such fragments, and gene products corresponding thereto.</p>   |           |  |

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# HUMAN NUCLEIC ACID FRAGMENTS, ISOLATED FROM BRAIN ADRENAL TISSUE, PLACENTA OR BONE MARROW

This invention relates to new nucleic acid fragments encoding gene products or portions thereof, which fragments are obtainable from human nucleic acid populations, individual members of such populations being present in widely varying amounts.

Situations are increasingly arising in which it is necessary to study complex nucleic acid or polynucleotide populations. For example, it is now widely appreciated that an invaluable resource could be created if the entire sequence of the genomes of organisms such as man were determined and the information available. The magnitude of such a task should not, however, be underestimated. Thus, the human genome may contain as many as 100,000 genes [a very substantial proportion of which may be expressed in the human brain (Sutcliffe, Ann. Rev. Neurosci. 11:157 (1988))]. Only a very small percentage of the stock of human genes has presently been explored, and this largely in a piecemeal and usually specifically targeted fashion.

There has been much public debate about the best means of approaching human genome sequencing. Brenner has argued (CIBA Foundation Symposium 149:6 (1990)) that efforts should be concentrated on cDNAs produced from reverse transcribed mRNAs rather than on genomic DNA. This is primarily because most useful genetic information resides in the fraction of the genome which corresponds to mRNA, and this fraction is a very small part of the total (5% or less). Moreover, techniques for generating cDNAs are also well known. On the other hand, even supposing near perfect recovery of cDNAs corresponding to all expressed mRNAs, some potentially useful information will be lost by the cDNA approach, including sequences responsible for control and regulation of genes. Nonetheless, the cDNA approach at least substantially reduces the inherent inefficiencies resulting from analysis of repeated sequences or non-coding sequences in an approach which depends upon genomic DNA sequencing.

Recently, the results of a rapid method for identifying and characterising new cDNAs has been reported (Adams, M.D. et al., Science 252, 1991, pp 1651-1656). Essentially, a semi-automated sequence reader was used to produce a single read of sequence from one end of each of a number of cDNAs picked at random. It was shown, by comparing the nucleic acid sequences of the cDNAs (or the protein sequences produced by translating the nucleic acid sequence of the cDNAs) to each

other and to known sequences in public databases, that each of the cDNAs picked at random, could be unambiguously classified. The cDNAs could be classified as being either entirely new or as corresponding, to a greater or lesser extent, to a previously known sequence. cDNAs identified in this way were further characterised and found to be useful in a variety of standard applications, including physical mapping. Unfortunately, such a process is insufficient. The longer the process is pursued with any given population of cDNAs the less efficient it becomes and the lower the rate of identification of new clones. In essence, as the number of cDNAs which have already been picked rises, the probability of picking a particular cDNA more than once increases. This difficulty is exacerbated by the wide range of abundancies at which different cDNAs can occur, which abundancies can vary by several orders of magnitude. Thus, whereas some sequences are exceedingly rare, a single cDNA type may comprise as much as 10% of the population of cDNAs produced from a particular tissue (Lewin, B. Gene Expression, Vol. 2: Eukaryotic Chromosomes, 2nd ed., pp. 708-719. New York: Wiley, 1980). The need to avoid missing rarer species in any given population presents a considerable problem.

Various approaches (so-called "normalisation" techniques) have been tried in addressing the problem of increasing the efficiency of examination of a mixed nucleotide population, for example, such a population as is to be examined in human genome sequencing.

Thus, a standard PCR protocol can be used to amplify selectively cDNAs which are present at extremely low levels, if there is information about the sequence of those cDNAs. If not, a primer specific to the desired cDNA cannot be constructed and the desired cDNA cannot be selectively amplified. The standard PCR method is therefore inadequate if it is desired to characterise a number of unknown genes.

A second approach involves hybridization of cDNA to genomic DNA. At saturation, the cDNAs recovered from genomic/cDNA hybrids will be present in the same abundance as the genes encoding them. This will provide a much more homogenous population than the original cDNA library, but does not entirely solve the problem. In order to reach saturation in respect of the very rare sequences, it will be necessary to use huge quantities of cDNA, which need to be allowed to anneal to large amounts of genomic DNA over a considerable periods of time. Furthermore, cDNAs which are homologous to genes which are present in multiple copies in the genome will be over-represented.



A third approach exploits the second order reassociation kinetics of cDNA annealing to itself. After a long period of annealing, the cDNAs which remain single stranded will have nearly the same abundance, and can be recovered by standard PCR (see Patanjali, S.R. et al., PNAS USA 88, 1991, pp. 1943-1947; Ko, M.S.H., NAR 19, no.18, 1991, pp 5705-5711). The methods disclosed in these two publications, however, suffer from notable disadvantages. They are entirely dependent on the stringent physical separation of single stranded and double stranded DNA, require an elevated number of manual manipulations in each reaction, and necessitate protracted hybridisation times (up to 288 hours in the method of Patanjali et al.)

Yet a further approach in "normalising" a nucleotide population is described in co-pending British Patent Application No 91 15407.0, filed 17th July, 1991 by MRC, and involves a PCR process in which a mixture comprising a heterogeneous DNA population and appropriate oligonucleotide primers is first formed and the DNA denatured, but before effecting a conventional PCR protocol the conditions are altered to allow the denatured strands of the more common DNA species to reanneal together, whilst avoiding annealing of primers to the DNA strands. By this means, rarer species can subsequently be amplified in preference to the more common species.

This PCR normalisation method in general comprises the steps of:

- (a) preparing a mixture comprising a heterogeneous DNA population and oligonucleotide primers suitable for use in a PCR process, in which the DNA is denatured;
- (b) altering the conditions to allow the denatured strands of the more common DNA species to reanneal, while preventing the annealing to the primers to the DNA strands;
- (c) further altering the conditions of the mixture in order to allow the primers to anneal to the remaining single-stranded DNA comprising the rarer DNA species; and
- (d) carrying out an extension synthesis in the mixture produced in step (c).

Advantageously, the method consists of a cyclic application of the above four steps.

It will be appreciated that the conditions may be altered by the alteration of the temperature of the reaction mixture. However, any conditions which affect the hybridisation of complementary DNA strands to one another may be varied to achieve the required result.

5 Because the reannealing efficiency of any given DNA species will depend on the product of its concentration and time, the more abundant the sequence the greater the extent to which it will reanneal in any given time period. Once a DNA species has reached a certain threshold  
10 concentration it will no longer be amplified exponentially, as a significant amount will have annealed to the double stranded form before the priming step. Thus, as each individual DNA species is amplified by the process to its threshold concentration, the rate of amplification of that species will start to tail off. Eventually,  
15 therefore, all DNA species will be present at the same concentration.

The length of the reannealing step will determine how much DNA is present at the threshold concentration. Preferably, therefore, the duration of the reannealing step will be determined empirically for  
20 each DNA population.

In the PCR normalisation process in general, the DNA primers may be adapted to prime selectively a sample of the total DNA population. By using primers which will only prime a sample of the population, only  
25 that sample will be amplified and normalised. The total quantity of DNA generated will thereby be reduced, which means that the cycling times can be kept low. This ensures that the method is applicable to complex DNA populations such as cDNA populations. In addition, a first primer can be used which is adapted selectively to prime a sample of  
30 the total cDNA population, and a second primer which is a general primer. Advantageously, the general primer is oligo dT (each primed cDNA will then be replicated in its entirety, as the oligo dT primer will anneal to the poly-A tail at the end of the cDNA).

35 In co-pending British Patent Application No 92 14873.3, filed by MRC 13th July, 1992, a new process is described which allows the study and identification of the individual members of a mixed or heterogenous population of nucleotide sequences perhaps of varying abundance. In preferred embodiments of the said process, the starting nucleic acid  
40 population is treated by:

(a) subjecting the nucleic acid to the action of a reagent,

preferably an endonuclease which has its cleavage and recognition sites separated, which reagent cleaves the nucleic acid so as to produce double stranded cleavage products the individual strands of which overlap at cleaved ends to leave a single strand extending to a known extent;

(b) ligating the cleavage products from (a) with a population of adaptor molecules to generate adapted cleavage products, each of which adaptor molecules has a cleavage product end recognition sequence and the population thereof encompassing a range of adaptor molecules having recognition sequences complementary to a predetermined subset of the sequences of the cleavage-generated extending single strands; and

(c) selecting and separating only those adapted cleavage products resulting from (b) which carry an adaptor of predetermined recognition sequence.

A preferred endonuclease for use in step (a) of the above process is Fok I.

An important feature of this process is the use of adaptor molecules. The adaptors used must have "overhanging" fragment recognition sequences which reflect or are complementary to the extending cleavage-derived sequences which the adaptors are designed to react with. It is also preferred that the adaptors used should end with a 5' hydroxyl group. The avoidance of a 5' phosphate group removes the risk of inappropriate ligation involving the adaptors.

Adaptor molecules may also contain a portion permitting specific sequence selection and separation (as in step (c) of the process) when a sequence is attached to the adaptor. For example, an adaptor can carry biotin, thereby permitting advantage to be taken of the biotin/avidin

reaction in selecting and separating desired adapted molecules. Additionally, adaptors preferably comprise a known and selected sequence such that specifically isolated adapted molecules can be amplified by known techniques (such as PCR) using a primer complementary to the core sequence.

Preferably the adaptors are short double-stranded oligonucleotides which can be joined to the ends of cleavage products. They will have been chemically synthesised so that their sequence can be predetermined

and so that large concentrations can be easily produced. They may also be chemically modified in a way which allows them to be easily purified during the process. As mentioned above, ideally their 5' ends will be unphosphorylated so that once joined to fragments the adaptor end of the latter will no longer be able to participate in further ligation reactions.

It is preferred that the adaptor cleavage product end recognition sequences are on the 5' end of the longest oligonucleotide strand making up the preferred adaptor molecules, are at least 3 nucleotides in length and with totally random bases at the single-stranded position(s) two nucleotides in from the 5' end. This then allows selection to be performed both during the joining reaction and during subsequent priming reactions. Then, because the final degree of selection is a result of the product of the degrees of selection achieved at these two stages, maximum selection can be achieved per adaptor/primer available.

Adaptor strand extensions on the 5' end of the longest oligonucleotide also facilitate the use of modified oligonucleotides for separation purposes. Preferably, the short oligonucleotide will be modified at its 5' end. This has the double benefit of requiring just one modified oligonucleotide for all possible single-stranded extensions that are used, and also placing the modification at a position where it cannot interfere with ligation or subsequent priming reactions.

Although only one type of adaptor is required per ligation reaction, it is preferred that adaptors covering all possible reactions in a chosen subset of sequences be present, because then the opportunity for fragments in the chosen subset to ligate to each other is minimised. It is also preferred that the chosen specific adaptor, carrying a predetermined recognition sequence, should not only be different from the other adaptors in its single-stranded extension, but also different in the rest of its sequence since this allows orientation to be introduced which is useful in subsequent steps. It is therefore also preferred that this adaptor has a modified oligonucleotide to facilitate its separation with the cleaving products to which it joins.

The above "adapting" process can be used to generate categories or subsets of sequences by making some of the adaptors specific in some way, and selecting and separating as in step (c). In this way subsets of sequences can be provided depending upon the specific adaptor

chosen, e.g. for use in subsequent nucleotide sequencing. This facilitates, for example, the identification of a large population of sequences by permitting a rational approach to splitting such populations into subsets, each of which subsets can be examined in turn.

In the light of these developments, the present invention now provides a nucleic acid fragment encoding a gene product or portion thereof and comprising any one of:-

- (a) a sequence selected from SEQ ID Nos 1 to 1193;
- (b) an allelic variation of a sequence as defined in (a); or
- (c) a sequence complementary to (a) or (b).

In another aspect, the invention provides a nucleic acid sequence as set out in any one of SEQ ID Nos 1 to 1193, or a complement or allelic variation thereof. Preferred sequences exhibit no more than 90% homology to a human sequence known per se.

In a further aspect, the invention provides a nucleic acid fragment comprising a portion of a sequence as defined above of sufficient size such that a probe of the same size and exhibiting complementarity to said portion can hybridise to said sequence. Preferably, such portions are at least 15 bases in length. It will be appreciated that minor mismatches in the aforesaid "complementarity" are not excluded provided hybridisation can still occur. In general, hybridisation conditions are within the choice of the skilled person, but reference can be made, for example, to the following: Melting temperature of hybrids - Bolton, E. T. and McCarthy, B. J. Proc. Natl. Acad. Sci, 48 p1390 (1962). Effect of formamide on lowering melting temperature - Casey, J. and Davidson, N., Nucleic Acids Res. 4, p1539 (1977). Effect of imperfect homology - Bonner, T. I. et al., J. Mol. Biol. 81, p123 (1973). General - Meinkoth, J. and Wahl, G. Anal. Biochem. 138, p267 (1984). Oligo hybridization and washing - Lathe, R. J. Mol. Biol. 183, P1 (1985).

The present invention also envisages DNA constructs comprising fragments or sequences as referred to above with a control or regulatory sequence.

The invention includes such DNA constructs using a gene system known in the art ligated to a sequence or fragment of the invention so as to enable, upon expression, the provision of a fusion polypeptide. Preferably, an endopeptidase recognition site is provided such that  
5 when the sequence or fragment is expressed it is expressed in frame with a known protein with the boundary being a cleavage site for an endopeptidase with a rare cutting site. The known protein can then be affinity purified, and the peptide corresponding to the fragment or  
10 sequence in accordance with the invention may be released by the endopeptidase. Alternatively, the whole protein can be used to raise antibodies which can then be screened for those directed at polypeptide corresponding to the fragment or sequence of the invention.

15 Since the present fragments and sequences can be used to produce, inter alia, corresponding genes, whether by isolating them, by synthesis or otherwise, such use and the resulting DNA fragments comprising genes are further aspects of the invention.

20 Yet another aspect of the invention is an expression vector comprising a fragment, sequence, gene-comprising DNA fragment, or DNA construct, as above, positioned such that that nucleic acid sequence which encodes the polypeptide corresponding to said fragment, sequence or DNA fragment is in operable reading frame with a control or regulatory  
25 sequence.

Other aspects of the invention are host cells incorporating a sequence, or fragment, or gene-comprising DNA fragment, or DNA construct, as above, as a heterologous part of the expressible genetic information of the cell. The production of such modified host cells can be achieved  
30 using methods known in the art. Such modified host cells can be used to express corresponding proteins, and these materials lend themselves in turn to the preparation of corresponding monoclonal or polyclonal antibodies using standard techniques.

35 Also included in this invention are such antibodies. Reference can be made, inter alia, to the following literature: Monoclonal antibodies, Cambell, A. M. Laboratory Techniques in Biochemistry, and Molecular Biology Ed. Burdon, R. H. and van Knippenberg, P. H. vol 13. Elsevier Amsterdam 1984. Goding, J. W., Monoclonal antibodies: Principles and  
40 Practice, 2nd Edition, academic Press, London 1986. Kipps, T. J. and Herzenberg, L. A., Handbook of Experimental Immunology : Applications of immunological methods in biomedical sciences, 4th edition Ed. Weir,

D. M. et al., p108 Blackwell scientific Publications, Oxford. Harlow, E and Lane, D. Antibodies, A Laboratory Manual, Cold spring harbor Laboratory, Cold Spring, New York.

- 5 Expression in an appropriate higher eucaryotic host may be important to ensure correct protein folding and also activity. Expression to avoid copurification of toxic products can sometimes be better performed in organisms approved for human consumption, eg prokaryotic *Bacillus subtilis*, eukaryotic yeast, mammalian cows milk vectors, and other  
10 methods known in the art.

The invention also includes novel gene products or portions thereof encoded by a fragment, sequence or gene-comprising DNA fragment of the invention.

- 15 It will be appreciated that the sequences of the present invention collectively have utility based, inter alia, upon their common origin, and hence they can effectively be considered together rather than as separate entities. It is convenient to represent them as separate  
20 sequences, because this is how they were produced and serves as "punctuation" between the different functional entities which each sequence represents. However, the sequences could just as easily have been presented as a continuous sequence derived by placing them end to end in the order in which they were produced, with a separate  
25 indication of where the beginnings and ends of the component sequences are.

- In contrast to investigations hitherto, where gene fragments (sequence fragments) could only be identified through some known characteristic  
30 [for example: their homology to a fragment which largely encodes amino acids identified by sequencing a previously isolated peptide or is the antisense of that coding sequence; or them having at least partial homology to previously characterised nucleic acids; or them having ability to encode expressed proteins which could later be detected by  
35 functional assays of the cells expressing those proteins or by using antibodies which had been previously raised against the proteins to detect their expression, Sambrook J., et al., Molecular Cloning CSH Press 1989], the sequences and fragments described by the present invention are entirely underivable and unpredictable from the prior  
40 art, but are nonetheless clearly of great value for various purposes.

Thus, such sequences, by comparing them to sequence databases, can be

used as a means for determining the existence of new members of existing gene families, new human genes when previously only non-human genes were known and new genes when previously no genes were known (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1980)). In all cases, this allows the isolation of the corresponding genes and their products, and hence enables the manufacture of molecules of potential biological interest by recombinant means. Screening libraries of known materials or hitherto unexplored source materials for biological efficacy is now an important industrial activity in the search for new therapies and therapeutics. When new sequences have already been found to have counterparts in gene families or in non-human genes then knowledge about biological efficacy may already be apparent. For example, new receptors or receptor agonists/antagonists may exhibit differences to known instances of these molecules, and such differences could make them more suitable as therapeutics by, for example, exhibiting binding characteristics which are more in keeping with avoidance of toxicity. Reference can be made, for example, to polymorphic dopamine receptors and the implications for mental health (Iversen, L. Nature 358, p109 (1992), and Van Tol, H. M. M. et al., Nature 358, p149-152 (1992)). Where absolutely required, realisation of full length cDNAs for expression can be achieved by using the sequences to screen (by hybridisation) suitable cDNA libraries containing full length clones (D'Alession, J. M., et al., Focus (Gibco B.R.L) 9 pl (1987)). Alternatively, the sequences can be used to design primers suitable for obtaining the missing sequences by PCR or other amplification methods (Frohman, M. A., Dush, M. K. and Martin, G. R., Proc. Natl. Acad. Sci. 85 p8998-9002 (1988)).

Appropriate use of the sequence fragments in antisense or triple helix (Griffin et al., Science 245 p967-971 (1989)) applications will be useful for identifying manipulable targets related to disease. For example, viruses have been inhibited by antisense RNA to their mRNAs (Chang, L-J., and Stoltzfuz, C. M. J. Virol. p921-974 (1987)). A similar effect could be achieved by targetting the expression of cellular proteins which are essential for growth or maintenance of the virus.

Partial or full length cDNAs have great utility once expressed. The manner of expression can be selected by one skilled in the art to suit the intended application. Expression of full length cDNAs is typically required for biological activity. Prokaryotic, and lower or higher eucaryotic hosts may be selected as the host for expression and higher



eucaryotes may be preferred to ensure correct modifications, for example, glycosylation in vivo, when this proves to be important. Expression can be ensured by situating the cDNA appropriately to signals for expression (Amann, E. and Brosius, J. *Gene* 40 p183 1985), Shimuzu, Y et al., *Gene* 65, p141 (1988), Straus, D. and Gilbert, W. *Proc. Natl. Acad. Sci.* 82, p2014 (1985)). Such signals may include a promoter for transcription, which may itself be regulatable.

The proteins thus-expressed can be screened for activities of therapeutic or commercial value. It may be that the proteins have to be first isolated for this purpose or can be assayed in situ. It may be desirable that some means of stabilising the expressed protein is employed. This can be achieved, for example, (and as indicated earlier) by expressing in frame as part of a fusion polypeptide (Smith, D. B., et al., *Proc. Natl. Acad. Sci.* 83 p8073 (1986)).

Useful antibodies can be raised against the expressed proteins. It is commonly not an absolute requirement that full length proteins are produced, although this may influence the quality of the antibodies produced. Peptides as short as 8 or 9 amino-acids in length can be used as antigens (Germain R., N. *Nature* 353 pp605-607 (1991), Rudensky, A., Y., et al., *Nature* 353 p622-627 (1991)). Immunogenic peptides could simply be synthesised using the amino-acid sequence translated from a sequence or fragment of this invention. It is desirable, although not absolutely required, that some means of producing purified antibodies is adopted. When fusion polypeptides are used to raise antibodies, an affinity matrix specific for the generic part of the protein allows the fusion polypeptide to be immobilised (Smith, D. B., et al., *Proc. Natl. Acad. Sci.* 83 p8073 (1986)). The immobilised polypeptide can then be used to affinity purify the antibodies. Antibodies to both the generic part of the fusion polypeptide and the part of interest are produced. When these need to be discriminated between, a different affinity column can be used to remove only those antibodies specific for the generic part of the polypeptide. Alternatively, and as mentioned earlier, it can be arranged that the boundary between the two separate protein components of the fusion polypeptide has the recognition sequence for an endopeptidase with a rare cutting site. The peptide of interest can then be released from the affinity purified polypeptide by the action of the endopeptidase (Nagai, K., and Thogersen, H., *C. Methods Enzymol.* 153 p461-481 (1987)). Another alternative is raise monoclonal antibodies against the purified protein.

The antibodies can be used for localising in situ, or quantifying in samples through, for example, ELISA or RIA assays, peptides against which they were raised. These uses are particularly beneficial when the results of the assays can be correlated to a disease condition, eg cancer. For example tumour markers may be found and used to target therapeutic agents. The antibodies can also be used to detect or monitor markers of undifferentiated growth, infection, cardiovascular or immune disease or a therapeutic response. When the antibodies recognise cell surface proteins they can be used in isolation or in combination to isolate particular populations of cells. These in turn can be used to isolate yet more cDNAs which will be enriched for yet more of such surface markers for the population, which, if similarly screened, will permit yet further subdivision of the population. Ultimately, panels of antibodies which can describe particular disease states will accrue. Such antibodies could be tailored for forensic applications as well as diagnostic purposes and disease monitoring.

The sequences or fragments can also be used for genetic analysis and mapping, for example, to diagnose the likelihood that a given individual is predisposed towards a given genetic disease. In the event of a sequence co-locating, genetically, with a disease gene, it can be used for the derivation of new disease therapies bases upon precise genetic knowledge. Such therapies can include, for example, the techniques of so-called "gene therapy" (Dusty Miller, A. Nature 357 p455-460 (1992)).

Antibodies can be produced against the protein of a genetic disease with sufficient discriminating power to discriminate between diseased and non-diseased states (Caskey, T. Genome Sequencing Conference, Hilton Head, S. Carolina (1991)). This would be useful for reducing the dependence of such tests on nucleic acid-based screens. Such antibodies also have the advantage of allowing detection of faulty expression of the protein, for example levels of expression which may be important for development of the disease in slow onset conditions.

Also very important is that not all cDNAs are likely to be found by conventional means, whereas the present sequences are, in one sense, "comprehensive". The use of the class of cDNAs which corresponds of necessity to truncated clones increases the chances that part of a cDNA will be cloned free of any sequences that could otherwise compromise it from being cloned. Sequence obtained can then be used to generate PCR primers from which the remainder can be obtained without having to

clone.

This invention will now be further described and illustrated by means of the following Examples.

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All oligonucleotides used in these Examples were synthesised Trityl on using an ABI 380B DNA Synthesizer according to the manufacturers instructions. Purification was by reverse phase HPLC (see, for example, Becker, C., R., et al., J. Chromatography 326, p293-299 (1985)).

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#### Example 1

Human brain and adrenal tissues were obtained from a mixture of 12 to 15 week menstrual age fetuses and then snap frozen in liquid nitrogen before storing in bijou bottles in a -80°C freezer. The two types of tissue were used separately, directly from the freezer, to prepare cDNA from which restriction fragments were generated for sorting into subsets. 1g portions of each of the separate tissues were homogenised, using an Ultra-Turrax T25 Disperser (Janke and Kunkel, IKA-Labortechnik), on ice in the presence of 4M guanidinium isothiocyanate to solubilise macromolecules. RNA was isolated from each homogenate by using centrifugation to sediment it through caesium trifluoroacetate. This was performed using the Pharmacia kit according to the manufacturer's instructions, except that centrifugation was performed for 36 hours and the RNA obtained was finally desalted and concentrated by performing two ethanol precipitations in succession with two 70% ethanol washes after each precipitation. In each case, polyA<sup>+</sup> (mRNA) was isolated from 200 to 400 µg of the total RNA by binding it to magnetic oligo-dT coated beads (Dynal). Solution containing unbound material was removed from the beads, which were washed, and then mRNA eluted directly for use. mRNA isolation was performed in accordance with the manufacturer's instructions. Yields of RNA from the beads were between 1 and 3% of the total RNA. 2 to 4 µg of the eluted RNA were used for cDNA synthesis. cDNA synthesis was performed according to the method of Gubler, U and Hoffman, (B. J. Gene 25 p263 (1983)) using a Pharmacia kit according to the manufacturer's instructions. OligodT was used to prime the first strand cDNA synthesis reaction. The cDNA was purified by extracting twice with phenol/chloroform and then low molecular weight solutes including nucleic acids below ca. 300 bases were removed by passing the cDNA reaction mixture through a Pharmacia S400 spun column used according to the manufacturer's

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instructions. Running buffer for the column comprised 10 mM TrisHCl, 1 mM EDTA, 50 mM NaCl @ pH 7.5.

5 The column eluate was adjusted to 10 mM  $Mg^{2+}$  and then the purified cDNA was restricted by the action of 1 unit per 10  $\mu$ l of the endonuclease Fok I at 37°C for 1 hour, so that it would be able to accept adaptors to enable fragment sorting.

10 The cDNA fragments were purified by two successive phenol/chloroform extractions followed by passing them through S400 spun columns as described above.

The adaptors used were oligonucleotides 5' N,N,N,N,TCCTTCTCCTGCGACAGACA (SEQ ID: 1194) with the complementary strand 5' TGTCTGTGCGAGGAGAAGGA (SEQ ID: 1195) and 5' AAN,N,TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1196) or 5' TTN,N,TCTCGGACAGTGCTCCGAGAAC (SEQ ID: 1197) each with the complementary 5' biotinylated strand GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198). These were added to 25% of the eluted material by incubating together 200 pmoles of the mixture of double-stranded adaptors in the elution buffer to which had been added  $MgCl_2$  to 10mM, ATP to 10mM and 0.025 units/ $\mu$ l of T4 DNA ligase. The oligonucleotide 5' biotinylated GTTCTCGGAGCACTGTCCGAGA, (SEQ ID: 1198) and whichever of the complementary oligonucleotides with which it was used, each comprised 1/32 of the molar proportion total adaptors. The final reaction volume was 90  $\mu$ l which was heated to 65°C for 3 minutes and then cooled to room temperature before the ligase was added. Ligation was performed for 16 hours at 12°C.

30 Two successive phenol/chloroform extractions were performed to remove the ligase. The final aqueous phase was passed through an S400 spun column (Pharmacia) as described above except that the column was used with 10 mM Tris pH 8.3/50 mM NaCl.

35 The column eluate was adjusted to 25mM  $Mg^{2+}$ , 0.5mM dNTPs in a final volume of 200  $\mu$ l. The mixture was placed in a thermocycler (Techne MW2) and heated to 78°C for 5 minutes. At this point 10 units of cloned Taq DNA polymerase (AmpliTag, Perkin Elmer) were added. This was followed by an incubation at 72°C for 10 minutes to fill in the unligated strand of the adaptor. After the second incubation 200  $\mu$ l of streptavidin coated magnetic beads (Dynal) prepared according to the manufacturers instructions were added to bind cDNA ligated to that of the oligonucleotides which was complementary to the 5'

.GTTCTCGGAGCACTGTCCGAGA (SEQ ID: 1198) biotinylated adaptor. Bead binding was allowed to proceed at 28°C for 30 minutes with mixing every 10 minutes.

5 Un-biotinylated cDNAs were washed from the beads with 400µl each of 2M NaCl twice, fresh 0.15 mM NaOH four times at 28°C for 5 minutes each, water twice and finally a buffer comprising 20 mM Tris pH 8.3, 50 mM NaCl, and 25mM Mg<sup>2+</sup>. The beads were then resuspended in 240 µl of the final buffer including additionally 0.5 mM dNTPs and divided into 4x60  
10 µl.

Four of the 60 µl aliquots, two from each tissue, were processed further specifically to prime and copy a subset of the immobilised, adapted fragments. 2 pmoles of the primer 5' CTGTCTGTGCGCAGGAGAAGGAA  
15 (SEQ ID: 1201) were added to each of two aliquots, one from each tissue. 2 pmoles of the primer 5' CTGTCTGTGCGCAGGAGAAGGAG (SEQ ID: 1202) were added to each of the other two aliquots. 2.5 units of Taq DNA polymerase were added to each reaction and 16 cycles of alternate denaturation at 95°C for 30 seconds, annealing at 63°C for 2 minutes  
20 and polymerisation at 72°C for 3 minutes was performed to accumulate the selected single-strands in solution.

On completion of the DNA synthesis reactions a further 30 µl of resuspended beads were added to each reaction to remove the  
25 biotinylated fragments. The reaction was incubated at 28°C for 30 minutes mixing every 10 minutes to ensure that the biotinylated strands were bead bound. Each aqueous phase containing the newly synthesised strands was then removed and extracted with phenol/chloroform twice to remove the enzyme before being further purified by passing through an  
30 S400 spun column equilibrated with 10 mM Tris pH 8.3/50 mM NaCl as described above.

Rounds of PCR amplification of subsets of the selected fragments were performed by using the original primer in each case, together with one  
35 of the primers 5' GTTCTCGGAGCACTGTCCGAGAG (SEQ ID: 1199) or 5' GTTCTCGGAGCACTGTCCGAGAC (SEQ ID: 1200). This simultaneously rendered the fragments double-stranded and increased the amounts of available material. It was not known how many cycles of amplification would be required at this stage, since each primer pair would be expected to  
40 behave differently. It was therefore necessary directly to determine a suitable number empirically by using standard agarose gel electrophoresis to examine the reaction products after a given number

of cycles. In some cases, to avoid the accumulation of non-specific products, it was necessary to perform an initial 5 cycles of amplification with both of the primers present at 2 pmoles each. All reactions were performed using 8  $\mu$ l or 12.5 % whichever was the larger but not exceeding 12  $\mu$ l of the column effluent above. Reaction conditions were adjusted to 20 mM Tris pH 8.3, 50 mM NaCl, 25mM  $Mg^{2+}$ , 0.5mM dNTPs and 2.5 units of Taq DNA polymerase in a final volume of 40  $\mu$ l. Apart from when an initial amplification with 2 pmoles of each primer was performed, 20 pmoles of each primer were used. Cycles of amplification were performed at 95°C for 30 seconds, 65°C for 1 minute and 72°C for 3 minutes.

For the purposes of cloning, selected cDNA was amplified as described immediately above, except that the reaction was not monitored. Instead, the number of cycles which had previously been shown to just give rise to all observable products plus another 4 cycles were performed. In addition, an extra 72°C for 10 minutes incubation was performed after the last cycle.

The products of the reaction were then prepared for directional cloning. Water was added to adjust the final reaction volume to 60  $\mu$ l. Enzyme was removed by two successive phenol/chloroform extractions. The final aqueous mixture was passed through an S400 column as described above, except that it had been equilibrated with 10 mM Tris HCl pH 7.5, 50mM NaCl.

For directional cloning, advantage was taken of the different known sequences introduced at each end of the selected cDNAs by the adaptors in a modification of the method of Aslandis, C. and de Jong, P. J. (Nucl. Acids Res. 18, p6156 (1990)). Different cohesive ends were produced on each end by using the exonuclease activity of T4 DNA polymerase to resect from the 3' end, to the first T in each case. To 75  $\mu$ l or 75 % of the column eluate, whichever was least, were added 9.5  $\mu$ l of 100mM TrisHCl pH7.4, 100 mM  $MgCl_2$ , and 9.5  $\mu$ l of 0.5 mM dTTP. 16 units of T4 DNA polymerase were added and the reaction incubated in a water bath at 37°C for 30 minutes. The enzyme was removed by extracting with phenol/chloroform, twice successively. The salt of the final aqueous phase was adjusted by passing it through an S300 column (Pharmacia) equilibrated with 10 mM TrisHCl pH 7.4, 1 mM EDTA as described above.

The E.coli plasmid cloning vector pBluescript KS+ (Alting-Meese, M. A.

and Short J. M., Nucl. Acids Res. 17 p9494) was prepared for accepting the resected cDNA by restriction cleavage at the BamHI and HindIII sites and then adaptoring the resultant cohesive ends using the specific adaptors produced by the oligonucleotide 5' AGCTCGGCTCGAGTCTG (SEQ ID: 1203) with its partially complementary oligonucleotide 5' GCGACAGACAGCAGACTCGAGCCG (SEQ ID: 1204) and the oligonucleotide 5' GATCCGGCTCGAGT (SEQ ID: 1205) with its partially complementary oligonucleotide 5' CCGAGAACAACACTCGAGCCG (SEQ ID: 1206). Preparation of the vector and adaptoring were performed according to standard procedures. Insertion of the cDNA was performed between the BamHI and HindIII restriction sites. Recombinant vectors were transformed into the host XL1-Blue (Bullock, W. O. et al Biotechniques 5 p376-378 (1987)) by the method of Hannahan, D. J. (Mol. Biol. 166 p577-580 (1983)). Suitable standard controls for the ligations and transformations were also included.

Post transformation procedures were as described in "Molecular Cloning", 2nd Edition (Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). Colonies were produced by plating onto X-gal/IPTG L-agar plates containing 50µg/ml ampicillin and 10µg/ml tetracyclin. Clear colonies were picked, each into a separate well of a microtitre plate, containing 100µl of L-broth and 50µg/ml ampicillin. Growth was allowed to occur for 16 hours at 37°C. 100µl of 50% or 30% glycerol was added to plates which were archived at -20°C or -80°C, respectively.

Bacteria corresponding to those archived were used for preparing templates for sequencing by the dideoxy method (Sanger, F. Milklen, S. and Coulson, A. R. Proc. Natl. Acad. Sci. 74 p5463-5467 (1977)). Bacteria for this purpose were either grown on L-agar plates containing 50µg/ml of ampicillin, prepared at the same time as they had been grown in liquid culture, or after plating out from the archive. Alternatively, fresh liquid cultures were inoculated from the archive.

In all cases, cDNA inserts were amplified for sequencing by PCR (Saiki, R. K. et al Science 239 p487-491 (1988)). PCR was either performed using bacteria directly added to the reaction, by a toothpick, or PCR was performed using 1/50th of the plasmid isolated by preparative methods (Holmes, D. S. and Quigley, M. Anal. Biochem. 114 p193 (1981)) from the bacteria in the liquid cultures or from the plates.

20 pmoles of each of the PCR primers 5' biotinylated GTAAAACGACGGCCAGT

(SEQ ID: 1207) and 5' CGAGGTCGACGGTATCG (SEQ ID: 1208) were used in 40µl reactions containing 2.5mM Mg<sup>2+</sup>, 50 mM KCl, Tris-HCl pH 8.3 and 0.25 units of Amplitaq (Cetus). Reactions were performed at 95°C, for 1 minute, followed by 35 cycles at 95°C for 30 seconds, 60°C for 30 seconds and 72°C for 40 seconds. After the cycles, a final incubation at 72°C for 5 minutes was performed.

After PCR, standard agarose gel electrophoresis was used to determine which reactions had been successful. The biotinylated strands of successful reactions were then recovered for single-stranded sequencing by binding them to streptavidin coated beads (Dynal) and then washing, all according to the manufacturers instructions, except that the washing steps were either performed manually or performed automatically in the 96 well microtitre plate format using a Biomek robotic work-station attached to a side-arm loader (Beckman).

Dideoxy chain termination sequencing reactions were performed using the immobilised, biotinylated strands as templates and 2 pmoles of the oligonucleotide 5' CGAGGTCGACGGTATCG (SEQ ID: 1209) as primer. Reactions were performed using fluorescently-labelled terminators (Du Pont) or a fluorescein-labelled primer (Pharmacia) according to the manufacturers instructions. Reactions were analysed using automated DNA sequencers. A Genesis 2000 was used for the "Du Pont" reactions and an A.L.F. for the "Pharmacia" reactions. Bases were assigned for the Genesis 2000 reads using the manufacturers Base Caller software. Files of called bases were then transferred to a SUN Network from an Apple Macintosh computer which had been used for base calling. Raw data from the A.L.F. reads was directly transferred to a SUN network where bases were called using the public domain "trace editor software" (TED). In both cases, files of called bases were entered into a Sybase™ database. Entering data entailed automatically removing vector and adaptor or linker sequences, but not editing ambiguous bases. After removal of the unwanted bases, files were automatically compared to other sequences in the cDNA database and the latest versions of the publically available databases, GENBANK and SWISSPROT. Searches were performed with the "basic local alignment search tool" (BLAST) (Karlin, S. and Altschul, S. F. Proc. Natl. Acad. Sci. 87 p2264-2268 (1990)).

Sequences SEQ ID Nos 1 to 610, given hereinafter, were obtained by the above procedure.

#### Example 2



A second method of preparing cDNA libraries for obtaining gene fragments of the invention took advantage of the PCR normalisation process described above. Standard procedures were used to prepare mRNA from RNA that had been isolated by standard caesium chloride bouyant density gradient methods from a full term human placenta. The oligonucleotide LNotdt, sequence 5' TACGTTTCGACAAGCTTGAATTCGCGGCCGC(T)<sub>x</sub>, (SEQ ID: 1210) was used at 1  $\mu$ M with AMV reverse transcriptase, to prime first strand cDNA synthesis under standard conditions from 0.5  $\mu$ g of the placental mRNA. Temperatures above 65°C were used to inactivate the reverse transcriptase and then the volume of the reaction made up to 100  $\mu$ l with water.

PCRs were then performed in reactions containing 1  $\mu$ l of the diluted cDNA, 10 mM Tris-HCl pH 8.3, 40 mM KCl, 1.5 mM MgCl<sub>2</sub>, 0.01% gelatin, 200  $\mu$ M dNTPs, 10 uCi a<sup>32</sup>P dCTP, 1  $\mu$ M each of the primers llAD1, sequence 5' GCC(TA)(GC)CGCCGA (SEQ ID: 1211), and LNotdT and Taq DNA polymerase. An initial denaturation period of 95°C for 90 seconds was followed either by 35 cycles of standard PCR, comprising 95°C for 30 seconds, 45°C for 30 seconds and 72°C for 30 seconds or alternatively 3 cycles of the standard PCR already described followed by 27 cycles of Cot PCR during which an additional step of 72°C for 16 minutes was placed between all of the 95°C and 45°C steps of the standard PCR. The standard PCR was followed by a single 72°C for 3 minutes step while the Cot PCR was followed by one standard PCR cycle except that the 72°C incubation was performed for 3 minutes.

Products of the PCR reaction were end repaired by adding 5 units of T4 DNA polymerase to the reaction and then incubating at 37°C for 10 minutes. Enzymes were removed by phenol extraction. The cDNA was precipitated by 70% ethanol, dried and then resuspended in NotI buffer. 20 units of NotI were used to digest the cDNA under standard conditions. cDNA was again phenol extracted and ethanol precipitated. 10% of the purified NotI cut DNA were ligated to the vector pBluescript lting-Meese, M. A. and Short J. M. Nucl. Acid Res. 17 p9494 which had been prepared as standard to receive this DNA by restricting with the enzymes NotI and EcoRV. Transformation and processing of clear colonies was performed as described above except that the host E.coli strain DH5a was used in place of XL-1 Blue.

Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced were performed as described in Example 1.

Sequences SEQ ID Nos 611 to 772, given hereinafter, were obtained by the above procedure.

Example 3

5 cDNA libraries corresponding to adult brain cortex (Clontech Laboratories, Inc., Cat No. HL10036) and adult bone marrow (Clontech Laboratories, Inc., Cat No. HL10586) prepared in lambda gt11 phage were transfected into E.coli Y1090 and plated out for colour selection of  
10 recombinant plaques ("Molecular Cloning", 2nd Edition Sambrook J., Fritsch, E. F., and Maniatis, T. CSH Press (1989)). 192 lambda Zap clones, corresponding to rhabdomyosarcoma cDNAs and a gift from C. Cooper, ICR, Sutton, were similarly plated except that the host XL-1 Blue was used.

15 Clear plaques from each library were resuspended in 5  $\mu$ l of Tris-HCl pH 8, 1 mM EDTA. 2  $\mu$ l of the resultant phage suspensions were added directly to PCRs for the purpose of amplifying the cDNA inserts for sequencing. PCR was performed as described in Example 1, except that  
20 the oligonucleotides used as primers for the lambda gt11 clones were 5' GGTGGCGACGACTCCTGGAGCCCG (SEQ ID: 1212) and 5' TTGACACCAGACCAACTGGTAATG (SEQ ID: 1213). Whichever of the oligonucleotides was to be used to prime the strand which would serve as the sequencing template was used in biotinylated form.

25 Preparation of clones for sequencing, sequencing and sequence analysis of cDNAs in clones thus-produced was performed as described in Example 1, except that 2 pmoles of the primers that were unbiotinylated in the PCR were used as sequencing primers.

30 Sequences SEQ ID Nos 773 to 1193, given hereinafter, were obtained by the above procedure.

35 The following are the SEQUENCE LISTINGS which comprise sequences SEQ ID Nos 1 to 1213 referred to hereinbefore. Certain of these sequences are preferred, and are listed as such after the main SEQUENCE LISTINGS.

21

## (1) GENERAL INFORMATION

## (i) APPLICANT

(A) NAME: MEDICAL RESEARCH COUNCIL

5 (B) STREET: 20 PARK CRESCENT

(C) CITY: LONDON

(E) COUNTRY: ENGLAND

(F) POSTAL CODE: WIN 4AL

10 (ii) TITLE OF INVENTION: HUMAN GENOME SEQUENCES

(iii) NUMBER OF SEQUENCES: 1213

## (iv) COMPUTER READABLE FORM:

15

(A) MEDIUM TYPE: DISKETTE

(B) COMPUTER: IBM PC COMPATIBLE

(C) OPERATING SYSTEM: MS-DOS

(D) SOFTWARE: EXTRACT

20

## (2) INFORMATION FOR SEQ ID :1:

## (i) SEQUENCE CHARACTERISTICS:

25

(A) LENGTH: 264 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :1:

GCCGATTCGT GACCAAGAAG GCTCTGTGCA TTCGGGTTTT CCAGGAGACT 50

35 CAAAAGCTGA AGAAGCGAAG AAGAGCCTTA AAGGCTGCAG CAGCAGCTCA 100

ATAACAAGC AAAGCGGAGG AACCCAGACA GCCCTGTGCC AAAGCCATAC 150

CAATATGATC TATCTTCTAA TGTATCCATG TTGTAATTAT ATATGTGTCT 200

40

GTGTGTGTCG AAATCTCTAG ACATACAGAT ATATATTCAT ATATCATATA 250

22

TATATATATA CACA

264

## (2) INFORMATION FOR SEQ ID :2:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :2:

15 AGGAACATGT GTTTATTCAT CCAGCAGTGT TGCTCAGCTC CTACCTCTGT 50  
GCCAGGGCAG CATTTTCATA TCCAAGATCA ATTCCCTCTC TCAGCACAGC 100  
CTGGGGAGGG GGTCAATTGTT CTCT 124

20

## (2) INFORMATION FOR SEQ ID :3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 333 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :3:

ACAGAGCCGA TTCTGCATCC ACTGTGGTCA ACATTTAGGA AGTTTTAAGC 50  
35 TAAGATTTGC CAAATTGTAG CCTACTGGAT TCCGGTTCTC TTGACATCTC 100  
TTTCTAGTAG CCATGTCTTG CACTTCCCGA GTATAAACGA ACTGAGATGC 150  
AAATTAAAAA AGGGAGGATT TAGAATAATG AAAAGAGAAA AGTCAAGAAA 200  
40 GCACAATCAC TAGTGTAGAG ATAACAGAAT TTCTGAATTC CCTGAAAGCA 250

23

ATCTATATAA ATGCATGTGA AATAATACAC CAGCATCTGT GGCCCATACG 300  
TCACATATTA GGAAGTATA ACATAAGGTA AAC 333

5 (2) INFORMATION FOR SEQ ID :4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :4:

AGGGAGAAAG GAACATCCGC GAACAGCCAA AGAAATCTCA GAAGAGTCCC 50  
GGAGCTCAAG GATCAGAGTA ACACAATTTT CACTTTTCT GTCTTTATGT 100  
20 AAGAAGAAAC TGCCTAGATG ACGGGGCCTC CTTCTTCAA CAGGAATTTC 150  
TGTTAGCAAT ATGTTAGCAA GAGAGGGCAC TCCAGGCCC CTGCCCCCAT 200

25 (2) INFORMATION FOR SEQ ID :5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :5:

ACAGAGCCAT TTGCATCCAC TGTGGTCAAC ATTTAGGAAG TTTTAAGCTA 50  
AGATTGCCA AATTGTAGCC TACTGGATTC CGTTCTCTT GACATCTCTT 100  
40 TCTAGTAGCC ATGTCTTGCA CTTCCCGAGT ATAAACGAAC TGAGATGCAA 150

24

ATTAAAAAAA GGGAGGATTT AAGAATAATG AAAAGAGAAA AATCAAGAAA 200  
GCACAATCAC TAG 213

5 (2) INFORMATION FOR SEQ ID :6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 345 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :6:

CGCAGGAGAA GGAACAGAGC CATTGTGCAT CCACTGTGGT CAACATTTAG 50  
GAAGTTTAA GCTAAGATTT GCCAAATTGT AGCCTACTGG ATTCCGGTTC 100  
20 TCTTGACATC TCTTTCTAGT AGCCATGTCT TGCACTTCCC GAGTATAAAC 150  
GAACTGAGAT GCAAATTAAA AAAAGGGAGG ATTTAGAATA ATGAAAAGAG 200  
25 AAAATCAAG AAAGCACAAT CACTAGTGTA GAGATAACAG AATTTCTGAA 250  
TTCCCTGAAA CAATCTATAT AAATGCATGT GAAATAATAC ACCAGCATCT 300  
GTGGCCCATATA CGTCACATAT TAGGAACTGA TAACATAAGG TAAAC 345

30

(2) INFORMATION FOR SEQ ID :7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :7:

25

TCCATTTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCTG 50  
GGGTTTTTTA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA 100  
5 GCCCAATACA AAATATATAG AAAAAGCGAT TATTACAATA ACGCTTCAAT 150  
TTCTTTTCC 159

## (2) INFORMATION FOR SEQ ID :8:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :8:

20

ATATTTCAAT CGAACAAAAA GGAACTTTT TTGAACTTA TTGAGGCTCT 50  
ACTTAAGTAC ATCGAAACCC TTAATGCTTC TGGGGCTGTG TTGATTTCTT 100  
25 TGCCTGGCTG GGGGTTTGAT TCGC 124

## (2) INFORMATION FOR SEQ ID :9:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 259 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :9:

CCGATACAAA TGTACGGAAT GTGTGAGTCC CTCTGGGAGC CCAACATGGA 50  
40 TCCGGATCAC CTGTTTGAAA CCATCTCCCA AGCCATGCTG AATGCTGTGG 100

26

ACCGGGATGC AGTGTCCAGGC ATGGGAGTCA TTGTCCACAT CATCGAGAAG 150  
GACAAAATCA CCACCAGGAC ACTGAAGGCC CGAATGGACT AACCTGTTC 200  
5 CCAGAGCCCA CTATATATTA TTTCTACTTC ATCTATATAT TGCAAAAATA 250  
GAAAATAGA 259

## (2) INFORMATION FOR SEQ ID :10:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :10:

20

GTCACCAAGA CCGAGGCCAA ACTGGGCACC TTCCCAGGG CCCTCAAGAA 50  
GCTCCTGCAC ACAATAAACG CGCCCTCGTT CTTTAGCAAG TCTGCTCCCT 100  
25 CGAGGCCACA GCAAGCCGGC TACGGAGCCC CCGTTCTGTT TTGAGCCGAA 150  
GACTACTTTA TTGGATGCGG TGAAAGGCCT CAGCTCTGAC ACTCTGATCA 200  
CTGTGACAAG GGGCCC 216

30

## (2) INFORMATION FOR SEQ ID :11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :11:



27

CACACTTCTT AAGATACATC AAGTACTAGT GATCTTTGCT AGCAGTTATG 50  
CCTGTTTCGT GTTACAGATT TGGCCATATA TTGACTAAAC AGCCCCCTGTA 100  
5 AAGTTGAAAG AAAAAGTTTA TAACAGTGAA CTTCTGAGGT TTACGTTACT 150  
GCAGGCTTTG TTGAGAAGAG ATTGTTACAG TGTGATTAT GGATGATCAG 200  
GGATG 205

10

(2) INFORMATION FOR SEQ ID :12:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 267 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :12:

TGCATCTGAA GAGTTGATGA TCGAGACTAC AGCTGCACTA TCAGACTGTC 50  
25 AGGCAGCTCC CTCAGAAACA GCTTCAACAG ACTGGCTGCT GAGCAGACAT 100  
CACCGTCCTT CCGAGCTCCA CGGCGACTCC ACTCTCGAAC TTCAGTCGAA 150  
GTTGTTCCAC CACCTTCACG TTACCATTCA CCCTAAAAGA CCTTCTTGGG 200  
30 TAAGTCCATG CTGCGTCAAA TATTCCACTA TATTCCACAC TACTGCTGGA 250  
TATGCCATTG TCGGTGA 267

35

(2) INFORMATION FOR SEQ ID :13:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :13:

5 GCCTCATCAG GTTTGCCCAG ATGCTGGAGA AGGTGTGCGT GGAGACGGTG 50  
GAGAGTGGAG CCATGACCAA GGACCTGGCG GGCTGCATTC ACGGCCTCAG 100  
CAATGTGAAG CTGAAC 116

## (2) INFORMATION FOR SEQ ID :14:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 296 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :14:

TTCGAACTTA CCAGCATCAT GTTGGTCTC TTCGTATGGT CAAACTTCAA 50  
CTTTATAAAA ATAGTGAATA CCACTTATTG AGTGCTTAGA GTGTACCAGG 100  
25 CATGGTGCTA AATACTCTCT ATCCATTATC TCATTAAATC ACATGACACT 150  
ATGAGAAATG TACTATTCTT ATACCCACGT TGCCCAGGGT CATACATCTA 200  
30 AGGGGTGCAA GGACCAGGCT TTGATTTCAA ATTATAATCT AATGCTCACT 250  
CTCCAGGCCT GATGTCACGC AGCTCCTCAT TCTTATACTT AACATA 296

## (2) INFORMATION FOR SEQ ID :15:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

29

## (xi) SEQUENCE DESCRIPTION: SEQ ID :15:

CGTCAGTGTG CTA CTT CACA TCATTAGCGA GGCCCAGAAA CTTGAACAGG 50  
5 AAGTCCGGCA CTACCAACAT GCCGCCACTC ATACAACTCA ACTCTTCCTC 100  
CAAAC TCGAT TCAAAGAGCA ATA 123

## (2) INFORMATION FOR SEQ ID :16:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :16:

20

CAACACATTA GTGCATCAAT ATGAATTACT TGTTTAAAAA ATCAAATGCT 50  
GGCATTGTCA GAAAAATTTA ACAGGTTTAT TTATAATTAT CATAAAGTTG 100  
25 ACGCTGAAAC TTGTTCACTG AAACATTTTA ACTTGCATTA ATGCTTTACG 150  
TCTCCGCATT TATATTAAAA ATTACACAC AAATGAAATG GAAAAACTGC 200  
CAATACCTGA TTTCTGTCCC TATTTTTCAC TCGCAATCAT ATACTTAGTA 250  
30 CTTTGTACTC TA 262

## (2) INFORMATION FOR SEQ ID :17:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :17:

5 TAGCCAAATT CTAGGGCATC CAGATGCATT TGAGCCAGTC GTAATCCAGG 50  
AAATGTCAAA AAAGCCCCAA TGAATGAACA GAAAATAGCC AGGAAAAATT 100  
TGAAAGTAAG TTTTGAAACA GGACTCGTGG AGATTCTAAA CCTTGCATT 150  
TCAAGAAACG TGCATCAGC 169

10

## (2) INFORMATION FOR SEQ ID :18:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :18:

AGGGGCACCA TTACCATCCA TCTGACATCG CATTTCCATA GAAATGGCCA 50  
25 AAGAAAGAAG GTCCTGGTAG GTTTTTCATA GAAAGACTCA AAAAGTTCAA 100  
CCTTTGATGC TATGCCCCAG CCCAATACAA AACTACACAG AACAAAGCAA 150  
TTATTAAAAT ACTGGCTTCG GTTCTTTTTT TTCCTTTGCA AAGTTTCCTA 200  
30 CATATATGTC TTTTACAGTA T 221

## (2) INFORMATION FOR SEQ ID :19:

## 35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :19:

5 TAGGCTCTGT GACGGCATAG TTTCAGTAG CTTATCACA ATATTCACAA 50  
TGGAGAATTA TATGACATGG TAGCAGAAAT AGGCCCTTTT ATGTGTTGCT 100  
TCTATTTTAC CTGAAATTGT AGATATAGGG TAATC 135

## (2) INFORMATION FOR SEQ ID :20:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :20:

20

GTTATCTATC TATCTTGCAG TTACCTATC TGATCTGATC TCTGTAATTA 50  
TAGTTCTGTC ATTTAAAATA TACTATTTAA ATCTAATTTT TACATTTCAA 100  
25 AAATTATCTT CAGTAGTAAC TAAGTATATT TTCTGTGGAT TCTGAGAATG 150  
TTATTTTTCA GAATGTGAGA GTACATATGT ACATTTATAA TCTTGTGACT 200  
TTAAAGTCTG TTTCAGATA CAGTATGTAA ATACTTGTAA AAAAAATTGT 250  
30 ATAATTTTGT GATAATGTAG TTTCCCAAAA CACATTTAGA AAGCATTATG 300  
TTATTAGTAA ATGA 314

## 35 (2) INFORMATION FOR SEQ ID :21:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :21:

|    |  |     |
|----|--|-----|
| 5  | TCTTCGCATC ACGCAGTACA GATACTCTTT CTGTACTTGC TTAATCTGCT | 50  |
|    | TTTTGGCATC AGTCAGTTCT CTTTCAGGTC AGCATAATCT TCTTCCTTCC | 100 |
|    | TCTGAAGATC TGCTTTCAGA TTCTGGGTAC GAGCAGAGCT TACAGAGAGT | 150 |
| 10 | TCCTCTTTCA ATATTTCTGT TTCTTGCC                         | 178 |

## (2) INFORMATION FOR SEQ ID :22:

## (i) SEQUENCE CHARACTERISTICS:

|    |                            |
|----|----------------------------|
| 15 | (A) LENGTH: 188 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :22:

|    |  |     |
|----|--|-----|
| 25 | ACATCTGATA TCCACCTCCA TGACAGACTG ATCACACCTC CTTCTATACT | 50  |
|    | ACTTCTGTTC TTTGTAAATA CTTAGTATTT TCCAAGGGAG TGTGAGAGAA | 100 |
|    | GAAATGCTAG GTTCATGAAG GGTCTCTAGG TTAAACTTTC TTTCTTTTTT | 150 |
| 30 | TTTCTTAAAA CAACACACTT ATTATCTTAC AAATCTGT              | 188 |

## (2) INFORMATION FOR SEQ ID :23:

## (i) SEQUENCE CHARACTERISTICS:

|    |                            |
|----|----------------------------|
| 35 | (A) LENGTH: 152 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

40

33

## (xi) SEQUENCE DESCRIPTION: SEQ ID :23:

TTCCANCTAA ACATCCAATA TNTCNTTTAN TGCTTTTATA TTTTNNAAAT 50  
5 GTTAAAACCC CTATACCACC TTTTGGGAAT GTTTTAAAT CTCCAATTT 100  
TCGTTATATA GGATCAACCA ACTAAGAAAA GATTTTATCA ATTGAATTGA 150  
GG 152

10

## (2) INFORMATION FOR SEQ ID :24:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 83 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :24:

ACAATACAGA GGACAAAGAC CCCTCACAGA ATGCTTTTCA ACCAACTTCA 50  
25 ACTTTTGCAC ACTTTTTCOA CGGTCCCACC ACA 83

## (2) INFORMATION FOR SEQ ID :25:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 176 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :25:

AAATGTCCAT TGCTGTATTG CGTGACCGTG GTCCTTGCCT GTCAAATNCA 50  
40 ACAATGACCA AATGATGATG CGCCCTTAAT ACCAGGATGA GACCAAACCT 100

34

ACACATCTCC CAAGTGCCGA ACAAAAACCT GAACAAAAAC CATNTGCACC 150

CTACATCTGG CTGACATTTA CATTTT 176

5 (2) INFORMATION FOR SEQ ID :26:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :26:

AAATGTATGA TCAGAAAATA GGTACGCTTT TAAAATATTT GAACAGAAAA 50

GCTACAAATA AATNGAGCAA TGCTTTTAAA ATCATCTTTG TTTTATAGAC 100

20 TTTTCTCGC ATGAATTACA TTTTACAATT TCATNNGGCA TATTCGCACT 150

TTAAGTACTG ACGAAGAAGA CTAAACAAT CATTTTTTAA CAATATTTAA 200

25 AAGGATCATA TAGTCGACTT TTAAACANC CC 232

(2) INFORMATION FOR SEQ ID :27:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 192 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :27:

GAGAAAGTCC TTGCCATTCT AAAAGCCACC CCACTTCTCT AAGGAGAATG 50

40 GCCCAATCTT CCCAAGTCCA CACAGGAGGG AACATTGTT TGCGTAAATA 100



35

CGCAATGCAA AATTTNNTAT CTTGGCTTAA TACNNCGACG TTTTATTTTCG 150

AATGATGAGC CTCTGCCCC CCCTTCCCCT TTNNNCTCCC CC 192

5 (2) INFORMATION FOR SEQ ID :28:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :28:

TAACACTTTA ANCATCTCTC CAAGCCAAGG AGGCTATGAC ANTGTAGCTT 50

TTTACTGTC CCCATCGGCC ACAATAACAA ACTTTTAACC CTCATAAAAT 100

20 GAATGAAATC ATCTTTCTAA GAATCTATAC CTACAATTCT CTGAACTAAT 150

CAATGAAAAA GATGATCAAT TCTGACTAAC AAAGATATAT CGATTCCATT 200

25 T 201

(2) INFORMATION FOR SEQ ID :29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :29:

AACCTAAGGC AGTTGACCCC ACCTTCCAAC ATGTTTTTCAC TTTATTGGCC 50

40 CCTCCCTACA TTCGGGTTAG GTTCCATTG ATTGACACAA TAATGACTTT 100

36

ATTCTCTTT GATCAGGATT TGGCACATAA AATCCTTTTA TCATAGAACT 150  
AACTATTTTA ATTACATATA ATGTAATAA TGGAGAGATT TATAGAGAAT 200  
5 TTTGTTTTTT TGTCATATAC TCCATTTCGA AGACAGATAT GATAGAACTA 250  
GAAATTAAGT TGCATTCTG CAAGT 275

## (2) INFORMATION FOR SEQ ID :30:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :30:

20

GTAAATNTAC AAAGATAACG TCGCAATTTT CTTAGATTTA AATCAAAGAC 50  
ATTCATCAAC AAGATTTTCGA ATGGAATATT CCAGAAATTT CTGAGCCATC 100  
25 TGATCACAAC AACCGTCTTT GA 122

## (2) INFORMATION FOR SEQ ID :31:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :31:

GGATTGNAG CTTGAAGTTC AGAGCTGGTT TACCCAAAAA GGGAGCCAAT 50  
40 AGAGATCTTC CCAATGAACC TCAATACACG ATCGTAATAC TCGCACAATG 100

37

AAATGTTAAG TATGATTCTA GACTTCACTG ACTATCACAA TGATATTTTC 150

TCGATCGCAC TAGTGCACAA CAAAACACGA TGAGTGCAAT GTGAAAC 197

5 (2) INFORMATION FOR SEQ ID :32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :32:

ACAAAAGTCT GAAGAAATCA CCAACNACAA GACGATTAGA AAATATGTTG 50

TTGGGGTCAC AACTAAAAAG TCCCTGATCT ACATTGNNTT TCNACTC 97

20

(2) INFORMATION FOR SEQ ID :33:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :33:

CAAATAAAAC AANTNTTGTA AAGCTACAAT AGTTATATAC CAAAGCAATA 50

35 CCTATTACAT GCTTTACACA ATCCCATGAA AAAATAATTT AATAGCTCCT 100

AATCCCTGAT GCAAGGCACT TCAAAGCACC CGCACAAAAC TCCATGAAAC 150

AACATACAAT ACATCATTTA AATAACATAA ACGACTTTCA CACACTTGAC 200

40

CTAGGAAAAA ATAAAATCCA TACAACCACA GCTAAAAACA TGTTAAGATT 250

38

CACATAAGA

260

## (2) INFORMATION FOR SEQ ID :34:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :34:

15 GGACNTGCGC NNNANNNANA GCCANTGAAC NCAGCCACCA NTGCAAGAAG 50  
ACTGCCTCTT NCCAGGCAAG ATTTTACTGG AGCAACANAA CCGGAGGTGT 100  
GATCCAAAAT ACCTTCCTTN CCAAGCCCGG GGTNNNGAT AAGGTGTGGA 150  
20 NTTNGGTAA AGACAAGG 168

## (2) INFORMATION FOR SEQ ID :35:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :35:

35 CTCGNACACT GTGGAGAGCC TCGNNNNNN NNGGTNTACT CAGGGGGACG 50  
AAAAGGAGNN GAANAAGTGA CACNGCNGNT AGCAGAGNGC ACAGAGCTGT 100  
GCTNNNGTGG TCCCTTAGNA CCCGAGNAGG TGGGCGCGAG GTGAANAAGG 150  
40 TGCNNGTGCG AGAGTGCGTG ATT 173

39

## (2) INFORMATION FOR SEQ ID :36:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 134 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :36:

AGCAAGTNNN NNNNNNCATC CTGAAAGTCA AAATGGAATT TGTGTTTATA 50  
15 CAACTAATAA TGATTTTTAT TTGCTCAGTA CAGACTNATT TACAATGAAA 100  
GTTTGTCTAA CCTTGGTAAG CTTGTTTACC GTTT 134

## (2) INFORMATION FOR SEQ ID :37:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :37:

30

TGGCGCCTGT CCGAGAGCAA GTNGNNNNNN NNCCTGAAAG TCAAAATGGA 50  
ATTTGTGTTT ATACAACTAA TAATGACCTT TTATTGCTC AGTACAGACN 100  
35 GATTTACAAT GAAAGTTTGT CTAACCTTGG TAAGCTTGTT AACCGTTTAC 150  
ATGACTTCTT 160

## (2) INFORMATION FOR SEQ ID :38:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 base pairs

40

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :38:

|  |     |
|--|-----|
| CTAGTTTAAT GAATCTGAGG GGCTACTATA AACAATCCCA CCCTCACACG | 50  |
| ATTTTTTACC TTCNTTACTT NGCCCTTCAT TAGGCAACCC TAGCAGCACT | 100 |
| CCACCTCTAT TCTCGCACTG TCCAAGAGGC CCACCTAATC            | 140 |

## 15 (2) INFORMATION FOR SEQ ID :39:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :39:

|  |     |
|--|-----|
| AGCAAGTATC ANNNNNNNNN ATACATTGA ATTCAAGTG TTTTTTGTCA   | 50  |
| AATTGTACAG TGTGTCAATT GATCTTCAAG CTGNNGGTGC CTAGAAATGG | 100 |
| GNCGGTGTCT GTAGCCCTGG CATGTGCACA CGGAGCATTT GCCACCACCG | 150 |
| CAAGCAAAAA GTCTGGGNGA AGTTCACCAA NGNCAAGAA NATTANGGGA  | 200 |
| AAA  | 203 |

## (2) INFORMATION FOR SEQ ID :40:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

41

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :40:

GAAAAGCNNN NNNNNNNGGC TTAAAGAACA ATATGCTGAG ATGGAGAAGG 50  
ACCTAGCGAA ANTNNNAACC TTTTAAGAAC TTGAANNACA ACAATCACAA 100  
10 ACTAATGAGA AGATGTTTAC CTCTCTCCTG AAAACTATGC CCACCAGACC 150  
GTTTAGCCTC TGCTCAAGCT 170

15 (2) INFORMATION FOR SEQ ID :41:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 270 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :41:

GCTGCATGTT TCCTGNATT TGAGCTTGAA AGTTCAGAGC TGTTTACCCA 50  
AAAAGGGAGC CAATAGAGAT CTCCCAATG AACCTCAAAC ACGTCGTAAT 100  
30 ACTCGCACAA TGAAATGTCA AGTATGATTC TAGACTTCAC TGACTCATCA 150  
CAATGATATT TTCTCGATCG CACTAGGCAC AACAAAATAC GATGAGTGCA 200  
35 ATGTGAAACA TCTACAAAGT AAATCACACA CTGTTTTTTT AAATNCATAG 250  
AAATTTGATT TGTAATAAAA 270

40 (2) INFORMATION FOR SEQ ID :42:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 245 base pairs

42

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :42:

|   |     |
|---|-----|
| AGAGCTGCAT GTTTCCTTGA TTTGNAGCTT GAAGTTCAGA GCTGTTTACC    | 50  |
| 10 CAAAAAGGGA GCCAATAGAG ATCTTCCCAA CGAACCTCAA TAACGATCGT | 100 |
| AATACTCGAC AATGAAATGT TAAGTATGAT TCTAGACTTC ACTGACTATC    | 150 |
| 15 ACAATGATAT TTTCTCGGAA TCGCACTAGT GCACAACAAA ATAGATGAGT | 200 |
| GCAATGTGAA ACAATCTCAA AGTAAATCAT ATACTTGTTT TCTTA         | 245 |

## (2) INFORMATION FOR SEQ ID :43:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :43:

30

|   |     |
|---|-----|
| TACTACTGNGA AAATGTACAA AGAAAGTATC CCCAAATNAT TTACAAAGCC | 50  |
| TAAATGTCCT TGATACACAT ACACGGNAGT ATGCAGACAA CAAAGATTAA  | 100 |
| 35 ATGAAGACAC TTTACTCTTT TCGG                           | 124 |

## (2) INFORMATION FOR SEQ ID :44:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double



43

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :44:

GAGTTCTCAC GAATACACAG GTTCAGAGAG ATGAGANGGA ANAACATAAG 50

GCAAATTCCT AACANNCGCT AATATAGGAG GCCGCTCGAT AGGATTTTAA 100

10

AAAAATAAAA ACAATCTTAA TAGTGGGACA AGGCCATCAG AAAA 144

(2) INFORMATION FOR SEQ ID :45:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :45:

25 ACTGATTCCNN NNTGAAAATA CCCCTTTTCT CCATTAGTGG CATGCTCATT 50

CAGCTCTTAT CTTTATATTC CAGTAAGTTA TTTGCTCTC ACTGTTTTAA 100

CAAAAAAAAA AACACAACA TAAAAATCCT TGCAAACCAT GTCAATTGGA 150

30

GAAATTTAAT GTTTTTCATA ACATGAA 177

(2) INFORMATION FOR SEQ ID :46:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :46:

ACTGATTCTG CGAAAATACC CCCTTTTAT TAGTGGCATG CTCATTCACT 50  
 5 TTATCTTTAT ATTCAAATAA GTTATTTTCG TTTCACTGTT TTAACAAAAA 100  
 AAAAAAAAAA AAAAAATAC AGCCCTCCCC AATCGAAGAT TTCAACTTTT 150  
 TAATTCACAC GGAAAAACCA AGACAATTTC ACAACTTCTG GACACAACCA 200  
 10 TCAACACAGG ACATTTTTTT TACAGGCAAA TCACTTAAAA CAAAAAGAT 250  
 CCCAGA 256

## 15 (2) INFORMATION FOR SEQ ID :47:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 base pairs  
 (B) TYPE: nucleic acid  
 20 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :47:

GAGAAAAGTC NNNNNNNNA GGTTAATCTA ACTTTTCTTG CTTATTTTCAG 50  
 CTATGATCTG AAAGGATGGA AGACACAAAA TGTATGNNTA AGGTATTTTT 100  
 30 AACAAAGATA CATGGGTAAA TTAACAGCAG TAATGTAAAA AAGACTGAGG 150  
 AGCAA 155

## 35 (2) INFORMATION FOR SEQ ID :48:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs  
 (B) TYPE: nucleic acid  
 40 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :48:

5 GCTTATTTTA CTATATCTAA AGGATAAAGC ACAAATGAT GAATAAGATA 50  
TTTNNACAAA GATACACG 68

## (2) INFORMATION FOR SEQ ID :49:

## 10 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :49:

20 CCTGAAAGCA AAGCCATNNA AAGCTTAGAG ACAAGCACNT GAGATGCAGG 50  
GGCCTAGCTA AATTNGAAC CTGNTGGAAC TTGAACCACA ACGATAAAAA 100  
ATTACAGAAG AGTTCACCTC TTTCTGAAAA CTATCCACAG ACCGTTTACC 150  
25 TCTGCTTCAA GCTANCAATA TATCAATGGC ACTCTCATAN CAGAAGAAAG 200  
AAGTTCCTAC TAGCTCCTGA TTATATTNAA GAAGATGCCC ATGG 244

## 30 (2) INFORMATION FOR SEQ ID :50:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID :50:

ACTCGNNCAG CGATAGTCGG AGCTACCAA CAAAACNCT NNNNCAGAAA 50

46

GGANAAAGNG CCGCCCTACG TGGTACACAC A

81

## (2) INFORMATION FOR SEQ ID :51:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :51:

15 GTACTTACTG CACTATGAAA AGCAATAGAT CGTCCATAAG TTATAACCAA 50  
AATCTCTCCC TCAGGAATAT ATTCCATACT ACTAACAGAC ATATTAAAAT 100  
TTAGAGATTT CACTTCTGTC ATAGTAGCAT GATCCCAAAG TCGAACAGTT 150  
20 TTGTCATCAG CAGAAAGAAT CTGTTTATCT CACTGCACCA CAGAGCTTTT 200  
TTATACCAGA AGNATGACCA CTG 223

## 25 (2) INFORMATION FOR SEQ ID :52:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 49 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :52:

TATGGTTTNT TGTAAGAAAAG CTCANNNANA AAGGGANNGG CTTAAGAGA 49

## (2) INFORMATION FOR SEQ ID :53:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 213 base pairs

47

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :53:

|  |     |
|--|-----|
| CAACGTCAGA GCACACNNNN NNCTCAGNGC ANAGGCATGA CAGGAGCTCA | 50  |
| TANCNATAAG CCATATAANN NTGTTACCTG TATAGAATGA TGAATTATCT | 100 |
| TTCTAGAGTC TATACCTACA GTTCTCTGAG CTAATCAATG GAAAAGATGA | 150 |
| TCAATCTGAC TAACAAGAGN AATTGATTCA TTTTCTTCCA CNCCCCTTCA | 200 |
| TTCAATAATC AAA   | 213 |

20

## (2) INFORMATION FOR SEQ ID :54:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 166 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :54:

30

|   |     |
|---|-----|
| GCGTGTTGTG NGGAGTGGNN GTCTNGTCNT CCTGTTAAGG TTTTGTGTG | 50  |
| CGTNNTTGCC TANGGGGNGG GTTNGGCAG GTGTTGCCGG TAGCNAAACN | 100 |
| GTTGGCCCCA TNGCCNGNAT TGNNNCCCN CNNGGGAANG GGGGGGNGA  | 150 |
| CCNNAGNGGG AAAAAA                                     | 166 |

35

## (2) INFORMATION FOR SEQ ID :55:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 base pairs

48

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :55:

ACCTCATAGC GAACTCGTCN TATAGANNNN ANNTGAGTCG AGCTCGATGT 50  
10 NGNCGTTGTN GCTGCCAAGC GACAT 75

(2) INFORMATION FOR SEQ ID :56:

- 15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :56:

25 AATNNNNNCC TATTTTGTA TTTTTTGAA AAAAGTTCAA TGTTCA GTTT 50  
TCCTTAGTTT TTACCTTGTT TTCTCTATAG GTCATGATTT CTGTGAAGCA 100  
AAAAGATGCC TTTTACCATG AATTCTTGAG TTTACATCAA TAATATTGTA 150  
30 TATTAAGGGG ATCAGAAGTA GGAAGGAAAA A 181

(2) INFORMATION FOR SEQ ID :57:

- 35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

49

## (xi) SEQUENCE DESCRIPTION: SEQ ID :57:

TCGAAGAGAC CTCAATCACC GTTTTTCAGG ATGTTTGATC ACAATACGAA 50  
5 GATGACGNNNA TCCAATTTCA GAACACCACA GGGCACTGGC ACACAGAGGG 100  
GATTATTACA GAACCACTGA GATGACATTT 130

## (2) INFORMATION FOR SEQ ID :58:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :58:

20

GTNATTTTGA AGGTCTCACA AATNTAAAGA CTTATTGTAG CCCATGAACA 50  
CATTGACAAG TACAAAATT ACAAAAATAT GCAGAAATAT TGAATAACTA 100  
25 GAACACAAGC CACTGTTTCA ACTCCAGAAA AAAGAAAGGC TTTACTTTTT 150  
CCATGAA 157

## (2) INFORMATION FOR SEQ ID :59:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :59:

40

GAGGTGAAGT TGTTCTTTAT TGAATTGCAT TATNAATGNA TAGGCTGTGC 50

50

CTTTTGNAC TCTCTATGAG TTCATGAATT TAACCAATAC GNCCACAAAT 100  
GCTGCTGCTG TCACAGAGAG ATGCCGATAA AGGACACCCA CCACCAATTT 150  
5 TTGAACAGGG AGGGGAGAAT CAACTCTGAA TGTGATGCAG TGACCAGGAG 200  
AGAGGACCAT GTTAAACAACA CCACACAAAT GCAAATGACT NGTTCTNAAA 250  
CA 252

10

(2) INFORMATION FOR SEQ ID :60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :60:

GACCTCGTTT TTCATCCTAT TATGGCGTTT ANCAGGCTAG ACAGAAACAC 50  
25 GCCTTAACTT TANTTGCCAC AAATCTTAAT ATTTTCTCCA CTAATATTAG 100  
AAAGGAAGCA ACAAATAATG TCGCTTTTCA CCTGACGTCT GGTCAACTT 150  
TCCGCCCAGC CTATTCCTGN GTCTTCCTCC TGCCTTTCTA ATGTCCCA 198

30

(2) INFORMATION FOR SEQ ID :61:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 229 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :61:



51

GAGGTGGCAT TATGTGAGAC AGCATTGGT TAGGGAGTGC CAAGCATTCT 50  
ACAGCATTG ATGGTGAAA TAGTCATGCT TTTTATTCT GCTCTCTAGG 100  
5 AATGTAAGGT GCACAGCAGG TCAGGGTACT GCTGTGTGAG ACAAAGGTC 150  
CAGGTAGAGG CAATTCCCCA GATGCAGGCA GGGCAGGTGC TCACTGGGCA 200  
GAGTGCTTCT CATAACCTT CAGGAACCC 229

10

(2) INFORMATION FOR SEQ ID :62:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :62:

CATCCTGGGC CCTGGCCGAT GTGCATATCA ACANAAAAAA GGGACTGAAG 50  
25 AACATCGGCC ATATCATCCA CACAAGCCAA ATCTCACACC TTTACTTTAA 100  
ACCGCTTAAT GAATTTTCATG ACCTTGAGGG CTAAAGATCG TTCTTCGGGC 150  
AAGAGCTTTT GGACTGTTTT TAGAACAGAA T 181

30

(2) INFORMATION FOR SEQ ID :63:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :63:

52

5 GTTGATTGTG AATCATCCCT CTAACATATA ATCAANANTA TGAGTAGAGA 50  
ATTGGCAGA AACAGAAAA GGACATGGGA TAACTTTTAG ATTTAAGAG 100  
GCAGGCTTG AACACAACT GGTATTCTGC TGACACACTG CTGCATATCA 150  
TAAGGCTACT CCACAAGACC ATTAGAAGTC 180

## (2) INFORMATION FOR SEQ ID :64:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :64:

20

ACAAATGTTCC AACATATATA TGGGGAGGGG AGAACANTTA TCTGTATAAC 50  
AGGGAAGTGT GATTATTTAA AAATANGCNA GAACTTATT CANCTGTGCT 100  
25 TTAGAAANAA NTGTATACGG 120

## (2) INFORMATION FOR SEQ ID :65:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :65:

CACATCGCTA TAATCCTTTC TGAGGACTTA AAACCTTATN CCACTTACCT 50  
40 TTATGACTTT TAACAAGCCT 70

53

## (2) INFORMATION FOR SEQ ID :66:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 240 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :66:

TTTCGAGCAA AATGTTTACA TTTACATGGA AATACACACT AAAACAGAAT 50  
15 ATTTTCCTAA TCATGAAACT TCGCCAAAGC AAAATACAAA CTTCCAACGG 100  
GAGGTCCACT CAACTAACAA CAATGATCCC CAAGCAGGGC ACCAAGAAAC 150  
CTGGGGGACC CTTTNCAAAA AACCTCCTTT CAAGAGACCC TAATACTCTN 200  
20 TCCACACACC CACACGATTT AGGAACTTGG ACATGTTTCCT 240

## (2) INFORMATION FOR SEQ ID :67:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :67:

35 GGAAGCACTA CATTTTCATCC AAAGCTGGGT TGAGTTATTT TTGAACACTT 50  
TACGATATGC TTAGGTAGGC TTTTAACTTG CTCCTCCAAA CAATATCTNT 100  
TGGGAAAACA AGCCCTGTGG AGAGATCCTT CCATCAAGTC GCTTCAATTT 150  
40 AACCTATTTC TAGAGGACTA GACATGCAGA ATCGTCAACT ACAGGGAATG 200

54

AAAAGTTCAA AAAGTAGATC CTACAAGATG AACGAGTACT TTTCTAAACA 250  
 TAAG 254

5 (2) INFORMATION FOR SEQ ID :68:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs  
 (B) TYPE: nucleic acid  
 10 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :68:

AGGCACCAAA GAAACACCAA GCAATAAAGT GAAAGACTAA CCAAGATTTG 50  
 ACATTGTATG NTTACTGTAT TCTTTAAGAA ACAACTACAA AAAGAAAATG 100  
 20 TCAACAAATN NNNACAACG AGAACCTGGG AATCCCGCA CGGAAGACAA 150  
 GAGATAACCT CTCCAATTGA ACACCGCTAG GNTTCTATNN TA 192

25 (2) INFORMATION FOR SEQ ID :69:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 base pairs  
 (B) TYPE: nucleic acid  
 30 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :69:

AGCAGCGNNN NNNNTNNAAC CAAAAGACAG GAGCAGAGAG GCCTGAGAGC 50  
 AGGAGGCGAA TTCGATCTCT CCTCACAAC AGCCCAGGAA AATATACACC 100  
 40 CCGGGGGAAG CC 112

55

## (2) INFORMATION FOR SEQ ID :70:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :70:

AAGGGTCTCC AATTTAATCC TTGGGTGTT TTACCACTTC TTTCGTAAAT 50  
15 TTATCAAGAT TTCTTTCGCA CAAATACTCT AGCGCCTCAC AACAAACCTG 100  
ACCTTGCGCA GGAAGTCGAC CATCAGCACC CCCTTTACAA CATCGTTCAT 150  
ATCACAATTG AGAAGATGAT GAATGAAGAT TCGCTTCCAA GTTCCAAGGG 200  
20 CAGATTTATT CCTTTAACTG ACATTTCCAT GA 232

## (2) INFORMATION FOR SEQ ID :71:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :71:

35 CNTGGATCCG NCCTTGTTAC GNCCAGGACG NCTGGACCGC AAAATGAATT 50  
TTCACTTTTT GACCACCGCC AGAAGAGATG ATTTTCTCAT CATNAACAAG 100  
GAACCTTTGA GGAGATCGAC TGAAGACTA GCGNCCCNGT CAGATAAGAT 150  
40 TTAGGGCTGA 160

56

## (2) INFORMATION FOR SEQ ID :72:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :72:

AAGGAAGACT GGTTCGCCAT CCGAGATCAT TAAAAANGNC TGACCCTAAC 50  
AATACGTACA AAAATATAAA ACGCAAATAA AAAATACAAA CAGATTCCTT 100  
CTTAAAGTAC TTTTAAGAAA AAAAGCAGGN CCTTGAAGT TTCGATTCTT 150  
TTTTCCTCCC GTCGCAAATT CTATGTTTGG AT 182

20

## (2) INFORMATION FOR SEQ ID :73:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :73:

CAAGAGGCAG CTGCCCCTCC CACCTCGGAG GNCTGAGAGG GNCTGTGNCG 50  
ATGAGCTGGA CGAGCACAGC ACTAAAAAGG CTTGCCCTNG CACAATAACA 100  
CTGAGAGGAT GATGAGAACA CNCTTGAAAT GCTTCATNCA CATGGGCAGG 150  
ANAGGCTGCA CAATGAAA 168

40

## (2) INFORMATION FOR SEQ ID :74:

57

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :74:

10

AACCTTTATT CATCCTCCTN TCCAAGACCT ATGAGAAGGT TCCAGGCCCC 50

AGGAACACAG GCTTCTTGGC CCCAGATGCA CCTCCCTGCA CCCCAGGGTT 100

15

GTATACCACA CCCCAGGGCCC CTAATCCCAG GCCCCGAGAT AGGAAAGCCA 150

ACTAGTTCTT TNNTGTGAT TCAGTAGGCC TGACCTATAG NTGGAATGTC 200

NCTNTCCCTN NAATAAATTN C 221

20

## (2) INFORMATION FOR SEQ ID :75:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :75:

AGACTGNTTG GGTCAATCCGA GATCATTAAT AATGNCTGAC CCTAACAATA 50

35

GGCACAAAAA TAAAAACGAA ATAAAAAACC TCCTTANNTT CGAAGTATCT 100

TAGAAAAAAA CAGGGCCTTG AGTTCTG 127

## (2) INFORMATION FOR SEQ ID :76:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs

58

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :76:

AAAAGAACAG CAGTTTCACA TTTCACATAT TTGAAAACA TTTCAAACC 50  
10 CTCTAATAAG TATTTAATGA AAATAAATTT ATCGAAGAGA AACAAATGACC 100  
ACAAAATTAA TACTACCAA TCATTACTGA GACTCTTGCA TTACAATATT 150  
15 TGGAGAGTAG GTGAAGAAAA TNTAGACCGA 180

## (2) INFORMATION FOR SEQ ID :77:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :77:

GATTAANNNN NNNGCACCCN NNATTACTGG CACAGCTGGT GAATATTTTC 50  
30 GTGGACTTTT GACTAGTGCA CCTGCGTGCG GGAAAACANT GATAAACTG 100  
TCACTTTAGC CNCNAACTAC AAGACCNGTT AGACTAGAGA GC 142

## 35 (2) INFORMATION FOR SEQ ID :78:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40



## (xi) SEQUENCE DESCRIPTION: SEQ ID :78:

5 GGCCCTGAGA GCAGGACGGC GAATTCGATC TCCTCCTTCA CAAACAGCCC 50  
ANGGAAANTA CACCCCGGGG AANNCCCCNC NCNNTTAGAA CCNNCAGGNT 100  
CTGNCCCCCC CNNGNCCCC CCG 124

## 10 (2) INFORMATION FOR SEQ ID :79:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :79:

AGGTATAGTG TTCCCTAATC ATGTACTTGT GAAGCACCCG GANTTTTCA 50  
TATAGTCTAA AAGCTAGAAG AACAAGAGTG TATTTCGTGG GTGGATGTAT 100  
25 NGTCACTTGC TGAANNNTT GAAATACCAT TATCCCCCTT GCTAACNCCT 150  
TTAAGNAAAN GCCNTTTTAA G 171

## 30 (2) INFORMATION FOR SEQ ID :80:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 98 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID :80:

CTGAACAGTG TGGTCGAGCA TTCCAAGTCC GTGAAGGTGC AGGAGCGGTA 50

60

CGACAGTGCC GTGNGGGCAC CATGGCACCT NGACCACGGG CNCCTAAG

98

(2) INFORMATION FOR SEQ ID :81:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :81:

15 CCTCAACAAG TCGGAGACCT GGGCGTCCAA CCTGCCTACA ACCACAGCCG 50  
CGAAAGAAGA AGACCTGCTG CTTCAATACA ACACGGGAGG ACCTGGCCAT 100  
CAACATCA 108

20

(2) INFORMATION FOR SEQ ID :82:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 180 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :82:

ACACATNACC CACNGCCAGT ATATCTCGAA CAAAGTCTCA GACGATACTC 50  
35 CCTAAATTG TAAAGCTTAA TACAGGTTNT GGAAATCATT TAACACCCGA 100  
GAATGTCCCA TCACAGTCTT CCGTCAAAT TTAGCCTCAC AACACAACA 150  
ACGCCTACGA AATTCTAAAT TCAGAAGGAA 180

40

(2) INFORMATION FOR SEQ ID :83:

61

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :83:

10

GGCTTCTGAT CGCCATCCTT GAACAGGGCA AAGGTGGCCT CACCAGCCTT 50  
CGATGCAGCT GCCATGCGCG CCAGAATCAG CGAAGGCATA CCCTTACGTC 100  
GTTGGACGCA TGTTTAGATG CCTTTGAGAC CGCCCAGAGA AGTCCTTGTC 150  
CTTCTTAATA AACACCTCCT CGCCAACTGC GACGACCACA ATCACCCTA 199

## (2) INFORMATION FOR SEQ ID :84:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 214 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :84:

30

CTTCGGTAGT GCCGCCGTGG TGCCACACAC CGTTGAGGTT GGAGTGGGCA 50  
CAGGCATGGT ACCACCAGCC TCCCCGCTGG TACAGGGCAC AGTTACCTGA 100  
GGGGAGAGAG AGAGTCCATG TCCTCTCACC AGAATAAAAG CCTCTACCTG 150  
CACCTCACAG TGCAAGGCTT TTGCCAGGCA TCCCCTGGCC CCTCCCATT 200  
NACNGAATAC AACC 214

40

## (2) INFORMATION FOR SEQ ID :85:

62

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :85:

10

CCTGGGCAAG CTGAATGTGA AGTTGACCAG GCTAACTGAG AAGCAAGCCC 50

AGTACCTGGG CATGTCCTGT GATGGCCCCCT 80

15

## (2) INFORMATION FOR SEQ ID :86:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :86:

GGGGATAGCT GGCTCATCCT CGGAAAACAG ACCCACATCT CTATTCTTGC 50

CCTGAAATAC GCGCTTTTCA CTGCGTGCT CAGAGCTGCC GTCTGAAGGT 100

30

CCACACGGCA TTGACGGGAC ACAGAAATGT GACTGTTACC GGATAACACT 150

GATTAGTCAG TTTTCATTTA TAAAAAAGCA TGACAGTTA TTACTCTGTT 200

35

TCTTTTAATG 210

## (2) INFORMATION FOR SEQ ID :87:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

40

63

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :87:

CACAAAAGC ATGATCAGGG CTAGCCTCAA TACAGGGAGA AATCATGGAT 50  
ATTTAAAAAT ACTTTTTTTG ATTCAGATTC CGGTATGACT GAAGANGCAA 100  
10 CA 102

(2) INFORMATION FOR SEQ ID :88:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :88:

25 GATAGGCGCA TGCATACTAC GGCTAAGGAG AAACAATGTT CCTACATATT 50  
ACGGGCAGTG AGAACATTAT CTGTATAACA GGAAGTGTGA TTATTTAAAA 100  
ATAGCAGAAC TTATCNGTCT GTGCTTTAGA AATAACTGTA TACAGTGTTA 150  
30 TAAGTTGAAA AGAACTCAAA ATAACATAA CAAATAAGAA CCTACGTATT 200  
AGAATTCAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAAAAAA 250  
35 TGACACAAAT TCAAAACACG ATCAT 275

(2) INFORMATION FOR SEQ ID :89:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 263 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

64

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :89:

GCCTGATGGT ATATACTGTT TTGCAATTGC ATACAACTGT GCATTACAAA 50  
TTAATAGTAA TTATGGTTTG GNGTAAAAT CGAGTTTCAG AATAAAATNA 100  
10 AAAACAATAA AATCCAAAGA ACGATGTAAA CAAAAAGCT TTTGTTTTGT 150  
TACAAAGTAT ATTAAGGATT TTCTGCTAAG ATTCAGTTTA AGAGTTTTCC 200  
15 TCGTGAAAAC TAAGTAGAAA CACAATGCCA ACAGCTGGCC AGTAATCAGT 250  
GCTGTGTACT CCA 263

20 (2) INFORMATION FOR SEQ ID :90:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :90:

GCGTCCTGCC CAACATCCAG GCCGTACTGC TGCCCAAGAA GACGGAGAGC 50  
CACCACAAGG CCAAGGGCAA GTGAGGCCGC CCGCCGCCCC CGAGGGACCC 100  
35 CTTTGAGA 108

(2) INFORMATION FOR SEQ ID :91:

(i) SEQUENCE CHARACTERISTICS:  
40 (A) LENGTH: 206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

65

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :91:

|    |  |     |
|----|--|-----|
|    | GCCTTGGTGG AGGGCATGAG GCTATGATGA CTATTGGCTA TAATATGGAT | 50  |
|    | ATGGCTTTGG CTGATAGATT TGAAGAGACC TCAATTACGT TTTTCAGGAA | 100 |
| 10 | TGTTTGATCA TAGATACAGA GATGGTGGTC CAGTTTTCAG AGCACCACAG | 150 |
|    | GGCACTGTGT ACACATGAGG GGTACCTTA CAGAGCCACT GAGAATATAT  | 200 |
| 15 | TAATAA   | 206 |

(2) INFORMATION FOR SEQ ID :92:

|    |                               |
|----|-------------------------------|
|    | (i) SEQUENCE CHARACTERISTICS: |
| 20 | (A) LENGTH: 210 base pairs    |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |
|    | (D) TOPOLOGY: linear          |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :92:

|    |  |     |
|----|--|-----|
|    | CCTTGGTGGA GGGCATGAGG CTATGATGAC TATTGGCTAT AATATGGATA | 50  |
| 30 | TGGCTTTGGC TGATAGATTT GAAGAGACCT CAATTACGTT TTCAGGAAT  | 100 |
|    | GTTTGATCAT AGATACAGAG ATGGTGGTCC AGTTTTCAGA GCACCACAGG | 150 |
| 35 | GCACTGTGTA CACATGAGGG GTTACCTTAC AGAGCCACTG AGAATATATT | 200 |
|    | AATAAANNNG   | 210 |

(2) INFORMATION FOR SEQ ID :93:

40

|  |                               |
|--|-------------------------------|
|  | (i) SEQUENCE CHARACTERISTICS: |
|  | (A) LENGTH: 189 base pairs    |

66

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :93:

|  |     |
|--|-----|
| AGGACTTCAT CCCAGACTCA CTTGTTCTGT TACAGAAACT AACCTAAAAG | 50  |
| GCTGGAAATT AAAGGATACA ACCTAAGAGG TTATAACAGC AGACTGGTAA | 100 |
| AACATGGCGA AAGGAGCTCT CTCTTTCCCC GCAGTCTACC AAGCTCCTGT | 150 |
| GCATTTTCAC CACATAGATC TGCTAGCTTA CAAATGATG             | 189 |

(2) INFORMATION FOR SEQ ID :94:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :94:

|  |     |
|--|-----|
| GAAGTGACAG GNAAGCTACA GGTGTATAAC AAATTTGTAA ACTAACCAAG | 50  |
| CACAATGTGG CAGGGCCTAG CTGCTACAAA GAAGACAATT TAACAAATAC | 100 |
| TCAACGCATG ACAAAAAACT CAGGACTGCA TTTGCACTAA TCGATAACGN | 150 |
| GTCATTTAAT   | 160 |

(2) INFORMATION FOR SEQ ID :95:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double



67

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :95:

TGCTTTATAC ATNATNAAAG GTAGGCACTT CATAAAATTT GCATTTTGGT 50  
AAAAGGCAAC AATTTGATGT CAGTATCTTA ATTGTGTCAT TAACTTTTTT 100  
10 AAGAGAACAG ATTATCAAAA TTTTACGAAG AAGAAAAAAA NTATAGTTTT 150  
TAAGGAAACT ACAGAAGGGA T 171

15 (2) INFORMATION FOR SEQ ID :96:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :96:

GTGGATAAGA AGATGTGTAC TTGGGAACAA GGCTAAAGCC ATTGGCTGAT 50  
TTCCCCAACC TTTTATTCG CGAAGAACT CCAGTTGTTA ACTTTTGTAG 100  
30 AGTTTTTTTT GGCAAAGAA CTNCATTAN C 131

(2) INFORMATION FOR SEQ ID :97:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

68

## (xi) SEQUENCE DESCRIPTION: SEQ ID :97:

5           GTCCTAATAT TTCTGTNCAG AAATTGTCAA CTTGACTTGA GAGTTGAGAA           50  
          GTAAAGTTAA GGCACGTACA ATATATCAGA ATGGAAGTCC TTAAGAGCAA           100  
          CTAACAGGTT CTTGATCAGA CTGACTATCT TTTCTTAAGT TCATAATATN           150  
          TTACTGTCCA GCCAACTATA CTTGGATCAA AATATCCTTC ATGAAGGGCC           200  
10           ATAATGTATT GATGATCTGC TGTAACCTTG AGAAGCTTCC TGAAGCTCNT           250  
          TTTGAATAAA TTTATNGAAC TTATGAAGA           279

## 15           (2) INFORMATION FOR SEQ ID :98:

## (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 266 base pairs  
          (B) TYPE: nucleic acid  
20           (C) STRANDEDNESS: double  
          (D) TOPOLOGY: linear

## 25           (xi) SEQUENCE DESCRIPTION: SEQ ID :98:

          GTGAGTCTTT CTTCAACTAG GGAATGTTT CCAGGGCAGC CCAGGCCTCA           50  
          CTCACGCAGG CCTCCGCGAC AACTGTTT CACTGACTGA GGATGAAGTG           100  
30           AAATCCTGAA AGCTGAGAGC CAGCGCCCTC ACACGAGGGC TGGGACGTAA           150  
          CAAAAGCCCA TCAAGAGTTT TGCCCAGGGC TTTCTTGAGC CTTGAAGCAT           200  
35           GACGAGACCA GGACCCTTTA GGATTAAGCA AGTTTTATGC GGTCTNAAAA           250  
          AACTCCAGGG CCTCCA           266

## 40           (2) INFORMATION FOR SEQ ID :99:

## (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 206 base pairs

69

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :99:

GGGAACATTT ATTGACATGA AAAGGTGTTT CAGATATACT GATATGTCAA 50  
10 ACAAATAGTA AAACAACATA GAGTAATGAT TCATTTTGGT AAAAAATATA 100  
TATGTATATA TAGAAAAAAA TTCTGCAGGA CATATGCTAA ATTGGTAACA 150  
15 GTGCTTACCC CTGGGAAGGG GGTATACGAT GTTGATTAC TCTTTGGGTA 200  
CGTATT 206

(2) INFORMATION FOR SEQ ID :100:

20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 73 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - 25 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :100:

30

CGCAACTNTC NCTAAACATC CAGTTTCTA ATNTAATAAA AAATGGCAGT 50  
AATTATCCTC ACCTCTCAGG GAA 73

35 (2) INFORMATION FOR SEQ ID :101:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 108 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - 40 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :101:

5 GAGCACAATC ATGNGCAAGC GCAACAGCAC ACCTTTATCC GAGTGAGACC 50  
ACTATGCAGC NGAACAGAGA CTCCTTATCT CTCCTTCTTG ATACTTGAAT 100  
ACTGCCCC 108

## 10 (2) INFORMATION FOR SEQ ID :102:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :102:

GAATTATCAA ACCATCNTTG CTGACATTAA TTTCCAGCT TTGATCTTAN 50  
NTCTNGCTTT AGTCCTCATA CAATGACTGT GTTTTCTCA AAGGATNTAT 100  
25 CGTATAGGNA TCCTTCTAAG CAATCCTGCA CCCACAAAAA AGCTGCATCT 150  
TCAATATAAC ANAAAAAGGN ATTTTGCAA AAGTACAAGT TTTATGTCTN 200  
30 CTGTTAAGTG 210

## (2) INFORMATION FOR SEQ ID :103:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :103:

71

CGTAGTTCGA TTCGAGTGGT CTATACAATC ACACCAAGCT TGATGTTGAT 50

GTCACCAAAA TTTCTTTCCA AAAAAA 76

5 (2) INFORMATION FOR SEQ ID :104:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :104:

CTTATGATTA ACTAAGCAAA TCTTTCATAG AAAGATATTA TCAAAGCTGA 50

AGAAATGCAA ACTTNAACAA AGTGCCGTGA GATTCCGGAA AAACCCTTAA 100

20 CCGATTGAAT GGTTTTTTAA GAATAAAAAA GAAGTCTGAT ACTGAACTAC 150

AAGTCGCAAG GAACATC 167

25 (2) INFORMATION FOR SEQ ID :105:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :105:

TATCTGCATA TCTAAACATA GAAAAGCACA ATAAAAACAC ATATCATAAC 50

CTCACGGGAC CACCATCATA CAGCAATTG TCATGATCAA AAGAAACATC 100

40 ATTAGTCGTG CCATAACTGT AT 122

72

## (2) INFORMATION FOR SEQ ID :106:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :106:

GAATTCTTCA CTCCAGATTT CCAATGCCAA GATACATTGA TACTGAACAT 50  
15 GGAGGCAACC AGGCCCGTTT CCTCCTTTCA AAGTCACCCC TCACAGACTC 100  
ATAATAATAT GCATGCCTGG GGGCAGGAGT CTGGAGCACC TATTCTNACA 150  
GATGATGTTA TTTACAAGTG TTTATGGATC ACTTGAAGAA ACTTGCTGTG 200  
20 TCCAGTGCTG CTGAAGTGC TAATAATGTT AAAGACACTT AAGAAGATGA 250  
AATAA 255

## 25 (2) INFORMATION FOR SEQ ID :107:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 227 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :107:

GGACGTGAAT TGGTGAATA TTTACAAAGA AAAGTGTGTT CTCAAAACAC 50  
TGTTCAATTGG TTGCAAGAAT GAATACTGAC TTCAGAACTC AAACAATGGA 100  
40 AGAACTTGCA TTTTATGGA ACTCAGTATT AAAAGAAAAT ATAATGTGAT 150

73

AGCACTTTGC AGATATGTCT AGACTGTGAT CTGAAGCATC GTAGTTTCCT 200

ATACCAAGAN ACANTTATGT GGTAAAT 227

5 (2) INFORMATION FOR SEQ ID :108:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :108:

GA AAAAATNGC ATGAAAGAAG ACTCTTNNNN NGCCATACCA TGGTACAATA 50

ATCATNAAAA NACAANAACA AAAACAAACA CATAAAACCA CTCACATATA 100

20 CATGTAGATA CAACAACNAT ATAATATCAA TAAAAAAAAA ATAGNAAAAA 150

AAAAAAATAA CA 162

25 (2) INFORMATION FOR SEQ ID :109:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 154 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :109:

AATTAAAAAT ATTAAACAAA ACTACCACTC CTCCTTATTA AAGCCCATAA 50

AAATAAAAAA CGAAACCCGA GAACCAAAT GAACGAAAAT CTTTCGCTTC 100

40 ATTCATCGTC CCCACAATNC CAGGCCTACC CCCCATACTG ATCATTCAAT 150

GTTT

154

## (2) INFORMATION FOR SEQ ID :110:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :110:

15 ATGTGCCAAG TAAAAAATCA ATNGTNGCC TTTTCCATT NCGCGGACAC 50  
CCATAGGCAC CAAAAAAGG TGCTAATAAG TAACATGTTT TAAGATGCAG 100  
AATAAGCTAT GGAAACAAGG AATGCTCCAA GTGTCCCAGT CTTTCTCCTT 150  
20 GCACTCCTTG TTAATAACAA TACACTATAT CA 182

## (2) INFORMATION FOR SEQ ID :111:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 94 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :111:

35 GAAGGTGAGA ATAGGTAGG GGAAACAGTA GGACAGGAAG TATTCACGTA 50  
CNTCAAAACC AATGGTAGAA CATCACATTT CAACTGCAA ACCA 94

## (2) INFORMATION FOR SEQ ID :112:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 92 base pairs



75

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :112:

10 TAGGGCAGTG AAACCTAATC TGCCTGATGC TATAANTGAN TGAATTACAT 50  
GNTCATTNGT TAAATTTTGT TCTAAACCCA TTAGGAAATT GT 92

## (2) INFORMATION FOR SEQ ID :113:

- 15 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 152 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :113:

25 GATTGTTTTT GCATTGCGTG TGTCACACAG CAGCACAAAG ACAATATATG 50  
TAAGCGTNNA TACACCAGAT TTGACACAAG AGATAGCGAA CACCACAAAG 100  
ATTAGGACAG ACCGCGTATA GTAGCTCTGA GGA ACTCAA GAATCTAGAG 150  
30 GG 152

## (2) INFORMATION FOR SEQ ID :114:

- 35 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

76

## (xi) SEQUENCE DESCRIPTION: SEQ ID :114:

TTGGCACTGA CATCCAGGAC AACAAATGCA GCTGGCTGGT GGTTCAGTG 50  
5 TCTGCAACGG GCCACTCCAG AACAGTACCA ATCCTGAAGG AAAATACNTG 100  
GCAGAAGGAG GCTGAGAAAG TGGCTCCGTG AAGGCNCTAT AGAGGGCTGA 150  
TCTGCCAGCA TGTCTTCAAT ATGAGGAAGG CA 182

10

## (2) INFORMATION FOR SEQ ID :115:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :115:

GGCACTGACA TCCAGGACAA CAAATGCAGC TGGCTGGTGG TTTCAAGTGC 50  
25 TGCAACGGGC CACTCCAGAA CAGTACCAAT CCTGAAGGAA AATACNTGGC 100  
AGAAGGAGGC TGAGAAAGTG GCTCCGTGAA GGCNCTATAG AGGGCTGATC 150  
TGCCAGCATG TCTTCAATAT GAGGAAGGCA NT 182

30

## (2) INFORMATION FOR SEQ ID :116:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :116:

77

50  
50  
100  
150  
200  
227

GAGGTTCTTG AATATGTATT TTTTACTGAA AAAATCATTG ATAAANTAAC  
ATACAAAAAT GTACAAACAC ATGAGTAAAT AATGTAATGA CAAAGGACTA  
TTTTCGGAAA AGTGTTTTTT AAAACANNCT AGATTTCAGT GCAAAAATGT  
ACCCCTGGCA CCTCTTAAAA CGTAAGAGCA AGCTCAAAAA CACGTAGTGA  
TGGAAATAAG CTAGCTACGC TCAATGC

10

(2) INFORMATION FOR SEQ ID :117:

(i) SEQUENCE CHARACTERISTICS:

15  
(A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :117:

50  
100  
150  
172

CGAGAGATTG GTAATGAGGA AGCAATTGG AGGGGNGGAA GCTACAANGA  
NNNNGGGAAT TACAACAATC AGTCTTCAA TTTGGACCC ATGAAGGGAG  
GAAATTTTGG AGGCAGAAGC TCTGGCCCCT ATGGCGGTGG AGGCCAATAC  
TTGCAAAACC ACGAAACCAG GT

30

(2) INFORMATION FOR SEQ ID :118:

(i) SEQUENCE CHARACTERISTICS:

35  
(A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :118:

78

AATGATGGAA GCAATTTTGG AGGTGGTGGG AGCTACAATG ATTTTGGGAAT 50  
TACAACAATA GTCTTCAAAT NNGGACCCAT GAAGGGAGGA AATTTTGGAG 100  
5 GCAGAAGCTC TGCCCCTATG NCGTGGAGGC CAATACTTTG CAAAACCACG 150  
AAACCAAGGT GGCTATGGCG GTTCCAGCAG CAGCAGTAGC TATGGCAGTG 200  
GCAGAAGATT 210

10

(2) INFORMATION FOR SEQ ID :119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :119:

GGTAAACACA AAGAGTTTCT GATAGTGTCT GCACAACAGC AAACCAACAT 50  
25 TTGGTGAGGA ATTAGCAATT TCTTGCCAAA GAAAATTGAT TCTGC 95

(2) INFORMATION FOR SEQ ID :120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 168 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :120:

GGAGTATTTN AANNTTTCAG ACTTTATTAC TTAATGAAAC AGTTTCTATA 50  
40 TACTGCTTCC AATATACTTT AATCCTTTTT TTCTCGTTAA ATTTTTTTTG 100

79

TTGTTCTTCA GTTGAGCTGA GATACTTTTA ATTACTTTTT ATTAAGTCT 150  
TCCAGAAACC GTAACAGG 168

5 (2) INFORMATION FOR SEQ ID :121:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :121:

GGAGTATTTA TCTTTCAAAC TCCNACTNA GTGAAACAGT TTCTATACCA 50  
CTGCTTCCAA TTACTANCTN TTTTNTCNGT TAAATTTTCN NCTGTTTTTC 100  
20 AGTTGAGCTG AGATACTTTT AATATNNNGT NACTGCTTCC AGAAACCGTA 150  
ACAGGTGCAG GAATAATTGA TGATATCCAA GTAGAGGCTG ATGNCAGCTA 200  
25 ATACATACTT CGGTGACNTT ATGCATCATG A 231

(2) INFORMATION FOR SEQ ID :122:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :122:

TCTATGGCAT GAATGTTTGC AACCAACNNN NNGGAAAGCC TTAAAGGAAT 50  
40 AGCTGTTTAC ATAGGAGACC GTGACAATGC TGTACGCAAT GCTGCACTAG 100

80

ACACCATTGT ACGGTGTACA ATGTCATGGG ATCAGGTGTT CAAACTGATT 150

GGAATCTTTC TGAAAAGGAT ATGA 174

5 (2) INFORMATION FOR SEQ ID :123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :123:

CTNNACAGGA GAAGNAAGTA ATGATCATTC CCCAAAATG TTCTGTTATC 50

AACTGNNTTT ATAAAAAATC GATTGTGGGT AGAAGCAGAG AAAAGGCACT 100

20 TAGTAAAGAT ACTACATGAN GAAAAANNTC TGCCCTTTGA ATTCTTANGA 150

AACATNNTNG NNGAATCAAT 170

25 (2) INFORMATION FOR SEQ ID :124:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :124:

AAGTAATGAT CATTCCCCAA AAATGTTCTG TTATCAACTG NNTTTATAAA 50

AAATCGATTG TGGGTAGAAG CAGAGAAAAG GCACTTAGTA AAGATACTAC 100

40 ATGANGAAAA ANNTCTGCCC TTTGAATTCT TANGAAACAT NNTNGNNGAA 150

81

TCAATNT

157

## (2) INFORMATION FOR SEQ ID :125:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :125:

15 CAACTTGAAA TACATTATGA TGTCTGATAT GATTAAATAT CATTGAGNAT 50  
CTTGCAAACA AAAAAAGCAA AAAATTAAAT CTCCATATCA ATCTTAAATT 100  
CTTGCCATAT TTACTTCTGG TAAATATTAC TTCTGGTCCT TATTCTATAT 150  
20 GTGTTATTGA AATTGTGTT 169

## (2) INFORMATION FOR SEQ ID :126:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :126:

35 GTTNGTTNN NNNNTGTTCC ACCTTTTGTT GAATTTTAGT TGTTAGGCTG 50  
AACCTCCGAG CAGTTTNAGG ACTTGCCTGA GTTTTCTTC 90

## (2) INFORMATION FOR SEQ ID :127:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 160 base pairs

82

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :127:

TTTAGTTTAC TTCTGTTCCA CCTTTTATTG AAATATTAGT TGTTAGGCTG 50  
10 AAAGCCTCCA GTTAAGAACT TGCTGAGTTT TTTTGTTTCA CCACTTGACA 100  
TTTACTATGC GCATTATATA NCTCAATTAT GTCTGTTTTT TATGCTAAGT 150  
15 AGGAAAACCA 160

## (2) INFORMATION FOR SEQ ID :128:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 150 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :128:

GCCCACAAC TACATCCTCA TTATTGGCGC CTACAACTC AACTACGAAC 50  
30 AACTCACAG TCGCATCATA ATCTTTTGAG GACTTCAAAC TTACTCGGCT 100  
ACCGCTTTTT GATGACTTCT AGCAAGCCTC GCTAACCTCC CTTACCCCCC 150

## 35 (2) INFORMATION FOR SEQ ID :129:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear



## (xi) SEQUENCE DESCRIPTION: SEQ ID :129:

5 AGAGAGACAG ACACCATGGA GCCACAGGGG CAAGAGGNG NTTCCGAAG 50  
CAGGGGANNG GCTATCACTC GGACGGACCN NNGCTCAACG AGTCCCACGA 100  
GAACACACCA GAAATTTGTC ATTGCACTCA ACCAAAATCG ATATCAGCAA 150  
10 TGAAAAACCC AAAACAGTTA CGANGCTAAT CC 182

## (2) INFORMATION FOR SEQ ID :130:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 219 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :130:

GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT 50  
25 TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGTC 100  
TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT 150  
30 TCAACCAAAA TCGATATCAG CAATGTAAAA ATCCCAAAAC ATNTTACCGA 200  
TGCTTACTTC AAGAAGAAG 219

## (2) INFORMATION FOR SEQ ID :131:

35

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :131:

AATAATTCAT CCACTTATGG AGGAGGAGGA GAATGTGGAA GAGGTAAAAA 50  
5 GCTGGGCACA AGTTCATATG CCTATGAGTC AGTAAAGACT GAAGTAATGT 100  
CCTATGTTGA GCTGGTTATT TTGATATATG ATAATAATTA TCTTTGTAGT 150  
AGAACATCGT TAACGGAATC ACAGATATAT C 181

10

## (2) INFORMATION FOR SEQ ID :132:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :132:

GACCAGCAGC TGTGGACATT ATGAGAAAGT GAAACCTGAG ATCCNCTGTT 50  
25 GATTGAGAAA TGCAACACCT CAAAATGNGG GACAGCTCCT GATTACCAGG 100  
TAGAAGATGN AAACAACCTGG GGTGTCCATT CAGGAGGAAA CAATTGCAAG 150  
CTAAGAAGTGT TTGAGAGTGA AGCTGCATTT TCTGNACC 188

30

## (2) INFORMATION FOR SEQ ID :133:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :133:

85

GAGGTTGGGT CGTTGCATCC ATCATCAGGA GTTGACTTGT TCTGAGCAAC 50  
TGAACAGAAC ACACCGCGAT GCTCTCGACA CTCCGCTCCT GGACTTCAGT 100  
5 CACGAGTGAG TTGATGGTGA CTTGACCTGA GAGATTTCAC AGAAGCTCTG 150  
TGAAGTGGTT GTGGAAGAAA TCTGAACTGT TCAAGTTAAC 190

(2) INFORMATION FOR SEQ ID :134:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :134:

20

ACATTACGAT CACTGATAGT TGGTGTGCGA CTGAAACCCA CATTNTGGTC 50  
AATCTCCTCG TAGAGCTTCT TCTTCACCTG AGGATTGGCA GCAGGAAGGC 100  
25 CAGGGTCCAT TTAATAAGA GGTGGTGATC TCCACGCCAG CCCCAGAT 150  
GTCCTTATA TGGTGAGAAT GNGTCATCTG AAAGCAGCTC TGAGTCTTGA 200  
TCTGGGCCAG CATTGCCATT ATTGAGTTTA TCTAG 235

30

(2) INFORMATION FOR SEQ ID :135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :135:

86

GAGAAACAGT ACCATCCANG ACACGATGTG GTGGAGGTTG ACNCCGCTGT 50  
ACCCCAGAGG AGCNCCACCT GTCCAAGATG CAGCAGAACA CTACAAAATC 100  
5 AACTATGTTT TTTAGCAGAT GCAGGACTAG ACCCCCACGC AGCTCTG 147

## (2) INFORMATION FOR SEQ ID :136:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :136:

GAAAAATGNG TTGANCCATT CATCCACAAA TTGACTGCC TGAACAACCA 50  
20 CCAAACAATA CACTAATGNT TCACACNTTT NCTTTTACTT GNACNTTAAG 100  
NTCCCANTGA GTCACGGTGA CTTACCCTAA ACATCTCAAN NGTNNTCTGA 150  
25 CTNAGAATGC GGAGGAGATC T 171

## (2) INFORMATION FOR SEQ ID :137:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 159 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :137:

ACATATATGT GGTAGGATAG AGAGATGGNN NNGTGATG ACATAGGTGT 50  
40 TTCTCGTGTG ATGAGGGTTT ATGTGTTATG TGGGGTGAGT GAGCCCATG 100

87

TGTTGTGGTA ATATGTGAGG AGTATAGGCT GTGACTAGTA TGTGAGTCT 150

GTAAGTAGG 159

5 (2) INFORMATION FOR SEQ ID :138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :138:

CCCACGACTT ACATCCTATN ACNCTTCGCC TAGCAAATA AACTACGAC 50

NCACTCACAA TCGCTCATAA TCTCTNAGG ACTTCAAAT NTCTCTNTGA 100

20 NCCTTTTGAT GACTTCTACA AGCCTCGCTA CCTCGCCTTA CCCNTGTNC 150

TNCGGGAGAA CTCTCTGTGC TGTACCAGT 179

25 (2) INFORMATION FOR SEQ ID :139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :139:

GACCTGGGAC GTAAATGATG AGACGGGTAC TTTGGCGGAC ATGAAGGAAC 50

TGGCATATGG AACCTTGGCT GTGAAGCTGC AGACTATAAG ACAGCATGAG 100

40 ACGACAATTC TGCTACTGCA ATGATGACAT CGTTTCAGAC CACAAAAGA 150

88

AAGGCGATGA CCAGAGCCGC AAGGCNG

177

(2) INFORMATION FOR SEQ ID :140:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :140:

15 GTTTACAACA TTTACATCCT ATGAACTCAT GGATTATAAA ACATTTGTGA 50

CTTATACTGT CTNTGTCAGT TA 72

(2) INFORMATION FOR SEQ ID :141:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 62 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :141:

30

GTNGGCTGAA ATGAAANAAT AAAACCAAGA AACGAATTGA AGTATTNGTT 50

TTAGTACGNA AA 62

35 (2) INFORMATION FOR SEQ ID :142:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :142:

5 ACCAGTNNNT GATTGGTAAA TGGGAAATAT AATTGATTCT GATCACTCTT 50  
GGTCAGCTTC TCTTTCTTTA TCTTTCTTTC TCCTTTTSTA AGAAAACGAG 100  
TTAAGTTTAA CAGTTTTCGA TTACAGG 127

## 10 (2) INFORMATION FOR SEQ ID :143:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :143:

AATATAAAG ACAGCAGTTT CACATTTCAC ATATTGAAA AACATTTCAA 50  
AACCCTCTAA TAAGTATTTA ATGAAAATAA ATTTATCGAA GAGAAACAAT 100  
25 GACCACAAAA TTAATACTAC CAAATCATTA CTGAGACTTT TTGCATTACA 150  
ATATTGAGAG AGTAGGTGAA GAAAATATAG AACAGAACAT GNACATTT 198

## 30 (2) INFORMATION FOR SEQ ID :144:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 174 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 40 (xi) SEQUENCE DESCRIPTION: SEQ ID :144:

GTTTCTCTNT ACGTCATCCA CCTTGACATG ATGGGTCAGA AACAAATGGA 50

90

AATCCAGAGN CAAGTCCTCC AGGGTGCAC CAGGGNNTAC CTAAAGCTTG 100  
TTGCCTTTTC TTGTGCTGTT TATGCGTGTA GAGCACTCAA GAAAGTTCTG 150  
5 AAACTGCTTT GTATCTGCTT TGNA 174

## (2) INFORMATION FOR SEQ ID :145:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 156 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :145:

GAGAAATAGT ACTTTAAAAT AAAACTAACA TGGTTTGATC AGCTTGAAAT 50  
20 AAGATTCATA AAATGTACCT TTTTGTATTG TTTTGTCTN GAGTTTTCGA 100  
TTGAGANCAT TTGGTAAAGA TAAAGAGGTT TCCTGGGTGG CAAAAATTA 150  
25 TTTTGG 156

## (2) INFORMATION FOR SEQ ID :146:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :146:

AAGATTCNNN NNTCCATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG 50  
40 GTTGGAAATT GGCTGTTTTG TTAAATATA TCTTTTAGTG TGCTTTAAAG 100



91

TAGATAGTAT ACTTTACATT TATAAAAAAA ATCAAATTTT GTTCTTTAAT 150

T 151

5 (2) INFORMATION FOR SEQ ID :147:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :147:

CTTTATTTTT CTTATACAGA TTCAGAGAAG TAAAANNCAG TACCAAATC 50

CAGGTAANNT GGTTTGATCT GATCGATTG GCTGCATACT TTCGGTACGT 100

20 ATAACATTCT AAACCTAAAA TAGAAATTTT TATATTACAA AACGAGGAAG 150

TAAAATTTTA AAAGTTAAAG TACTAGC 177

25 (2) INFORMATION FOR SEQ ID :148:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 148 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :148:

GATTCNNNNN TCCATTGAAT GTTACCTGTG CCAGAATTAG AAAAGGGGGT 50

TGGAAATTGG CTGTTTTGTT AAAATATATC TTTTAGTGTG CTTTAAAGTA 100

40 GATAGTATAC TTTACATTTA TAAAAAAAAT CAAATTTTGT TCTTTAAT 148

92

## (2) INFORMATION FOR SEQ ID :149:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 204 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :149:

AGATTCNNNN NTGGNATTGA ATGTTACCTG TGCCAGAATT AGAAAAGGGG 50  
15 GTTGGAATT GGCTGTTTTG TTAAAATATA TCTTTTAGTG TGCTTTAAAG 100  
TAGATAGTAT ACTTTACATT TATAAAAAAA ATCAAATTTT GTTCTTTATT 150  
TTGTGTGTGC CTGTGATGTT TTTCTAGAGT GAATTATAGT ATTGACGTGA 200  
20 ATCC 204

## (2) INFORMATION FOR SEQ ID :150:

## 25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :150:

35 AACATCGAGG TCGTAAACCC TATTGTTGAT ATGGATCTCT ATGAATAGGA 50  
TTGCGCTGTT ATCTCTAGGG AACCTCACCG TTGGCAAGTT ATT 93

## (2) INFORMATION FOR SEQ ID :151:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 151 base pairs

93

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :151:

10 AATCGAGAGA AAAAATGATG ACACTGTAGC AATATCGTCG GANTCCACCT 50  
ACTTTGGGAT CAGCCTATCC ATCCGTGTCT TCCTATTTAA ATCGTCTATC 100  
CTCTATCCTT CCCCTGTCTT TTTNTGAAAA GGAAAAAAC CAGGAAGGTG 150  
15 T 151

(2) INFORMATION FOR SEQ ID :152:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :152:

30 TCTGAGAGGA ATACTNNTAA GTGCAATGAA TATTGCAAAT TTTCCCCCCT 50  
CTAAGTAATT CCCGATATTA GCAAANCANN NANATTAATG TCCCAGTGAA 100  
TGTAGCCTC 109

35 (2) INFORMATION FOR SEQ ID :153:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :153:

5 AAAATTATTT TCACAGTCCC CCCCAACTCT CATTGCGTCG TTAAAGTCCC 50  
TCCAATCCTT TTTTAGTTGT GAAAAAATAA GGGGCCTTTA AAGGAGGAGG 100  
AGGAAAAGGG GAAAAAACC CATAATGGGC CTAAAA 136

## (2) INFORMATION FOR SEQ ID :154:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :154:

20 CATCTTCATC ACCATCACAA TACTCATCAT CACCACCCTT CATNCACTAT 50  
CATCTTCTAT GACTGCAAAC TTCTATCTT TCTCTTCATT ATAGAAAGTT 100  
25 TCAAGATGAG TATACGCATC TATCATTCGA ATTGTGTCAT TAATTGTAG 150  
GGCCTCATTG 160

## (2) INFORMATION FOR SEQ ID :155:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :155:

40 ACCAGTNNNN NNNGGTCAAA TAGGGAAATA TAATTCGATC TCTCGAATCA 50

95

ACTCTCTGGG TCAGCTTTCT NCTTNTCTTC TATCTTTNCT TNTCTCCTTT 100  
TTTTAAGAAA AACGAGTTAA GTCTTAACAG TTCTCGCATT ACAGGCTTGT 150  
5 GACTTCATGC TTACTGTAAA GTGGAAGTG AGATATTTTA A 191

(2) INFORMATION FOR SEQ ID :156:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :156:

CAACTGAACG CTTTGCTCAG GCTGCTACAA TGAAGGAAT TGNGGGCNAN 50  
20 TTGGTGGAAC TCCTCCTGCN NTCAACCGTG CAGCTCCTGG AGCTGAATTT 100  
GCCCCAAACA AACGTCGCCG ATACTAATAA GTTGCAAGTG 139

25 (2) INFORMATION FOR SEQ ID :157:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :157:

GGTACAGAGC ACTCTGTACC AACACACAGA ATTTACTGTT CTGCAAATGA 50  
CCAATACTAA AAATTTATAA AGATGTGCAC AATTNNNNGC AGGCAATCTT 100  
40 TCTTTTGTTT ACAAGATACA ACATTTAACA GTTATTAAAT GTAATCCTGA 150

96

AGCACCCGCA AATTACCTT TG

172

## (2) INFORMATION FOR SEQ ID :158:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 93 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :158:

15 GGGTGGCTGT TNNGTATATC TCGTTAGTAA ATGTACATGC TCTTCAGGTT 50

CTAGGGCTCC TGTTAGGGGA GGCAGAAATG TTGGAAGNGG GGG 93

## (2) INFORMATION FOR SEQ ID :159:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :159:

30

GNATTTTTTT ATTGATATAT CATAGTTGTA CAAACATTG GGAGTNCANG 50

TNGATACTTT GATACTATCG TGTNNNNNGG ATAATCACCA AATTGGATTC 100

35

CA 102

## (2) INFORMATION FOR SEQ ID :160:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 205 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :160:

|    |   |     |
|----|---|-----|
|    | GCTTTTNNNN NNNNNNNNNC AGGTTTATAT TTACAATAAT TATCTTCCTA  | 50  |
|    | TAGAAGCAAT AANN CNAGTA TTCTCCAGTA ACAACACANN NNNATATTCT | 100 |
| 10 | ACTCATCAGA GTTGGGAAAA ATAGGAATAA AGCAGATTCC ATACAGAAAT  | 150 |
|    | ACCGTACTCT GCATATGTAC AAATAAATTC AATATATTAA ATCATTTTGA  | 200 |
| 15 | GCGGA   | 205 |

(2) INFORMATION FOR SEQ ID :161:

(i) SEQUENCE CHARACTERISTICS:

|    |                            |
|----|----------------------------|
| 20 | (A) LENGTH: 150 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :161:

|    |  |     |
|----|--|-----|
|    | AACTTTTTTA ATGGGTCTCA AAATCTCTGA GACAAAATTA CTNNGNNNAA | 50  |
| 30 | AGTTGTTTTTC CATATAAAAA ANNNNNNTGA TTTTAAAAA ACTAANNAAC | 100 |
|    | TTAAAAACNT GCCACACGCA AAAAAAGAAA CCAAAGTGG GNCACCAAAA  | 150 |

35 (2) INFORMATION FOR SEQ ID :162:

(i) SEQUENCE CHARACTERISTICS:

|    |                           |
|----|---------------------------|
|    | (A) LENGTH: 77 base pairs |
|    | (B) TYPE: nucleic acid    |
| 40 | (C) STRANDEDNESS: double  |
|    | (D) TOPOLOGY: linear      |

## (xi) SEQUENCE DESCRIPTION: SEQ ID :162:

5 TATTCAAAAG AAAAACATGG GTAAAAATGA TAGTGTTAAA TCTTGGCTCT 50  
GTGTACATAG ATAGATACCT GTTACAG 77

## (2) INFORMATION FOR SEQ ID :163:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :163:

20 GAAAATTATT TTCACATCCC CCCCAACTTC TTGCTCTTAA TCCTCATCTT 50  
TTAGTTGAAG AATAAGGCTT AAGAGAGAGA AAGGAAAAAC CATAATGGCT 100  
AACTTAGCAG CACAACACGG TTCTTTTATC AAGGCGTNAT CATCATTTCT 150  
25 CAAACTGACA TGCTACAGAA ATGTCTTCCA AA 182

## (2) INFORMATION FOR SEQ ID :164:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :164:

40 GAGGGAGCAA AGAGAGCCAT AAAGGCTCGT GCTGGGAAAG AAAGCTGTTA 50  
TGCTTAGACT TCTCTAGGTG AACTCAGAGT CTTCAAAGAG GAAATGTTAC 100



AAATTGTCAC CCGCCAGCTT TCTGGCCAGT AAGCAGAATG CCAGGTTGCT 150

CAGATTCACA GACATTGCA AACAGAAGA TG 182

5 (2) INFORMATION FOR SEQ ID :165:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :165:

GTATCTCCCT CTACATCCCT CCCGAAATAC TAGGAATACT TATTCTATAT 50

GAGACATATA TACCACCCAA GTTTTAACAC CATATCCCAT CGGCTGTTAG 100

20 TGTATATAAA AAGAAATAA 119

(2) INFORMATION FOR SEQ ID :166:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :166:

35 GTACAAAGCC ACTCATCCTC GTGTGCCTAT CACGTTTTCC AACACATAG 50

GATCCCATCT CAGGAGCAGG ACCAGTGTTT AGCTAGATTA AACTTCGCTG 100

GTGATCTTGT TGATGCATAT AAAGTAATCT GGCATATATG GTTAAATTCA 150

40 AGATGTTATG GCAGAAGTGA CTTGTTTTGC TCAACAAGCA TTG 193

100

## (2) INFORMATION FOR SEQ ID :167:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :167:

GTTCTGACTN AGAACTGAGC ACATAGCATT GACGCGGTAC CCTTGGAGAG 50  
15 GGTGTGCTAG GAGGAGTGCT TGGCGAATTT GGACACGTAC TAATGTCTCT 100  
GAGCCAGTCT GAATCTCTGT GAAGATGCCC CAGTGGAGGT GGCTGAAGAT 150  
TAAATGGACA GTTTATAAAG TGTTCGGP GCCGA 185

20

## (2) INFORMATION FOR SEQ ID :168:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :168:

GGACAACACA GCACCCATCC ACTACCCATT CAGAATTTAT ATAGAATATG 50  
35 TACCCATGAT TATCTAGGTG AATCAATGCA ACAGTAGCTC TGATGTCCAG 100  
ATTTCCTAGT CTATTATTTT GTGTACAGAT CCTCTAACCA CTTAGAAATA 150  
ATTTTAAAA ATA 163

40

## (2) INFORMATION FOR SEQ ID :169:

101

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :169:

10

AGACAAATTC NNNNTNNNNN NTGCCTGATA ATTCAGATG CCACCGTATA 50  
GCAAAGGGTG AACATGTTTT CAACCCTTA ACTTTTACG GTGTTTGAAG 100  
ACCAGCTACT CCTTAATATT TATCAATGGA TTAAGAAGTT TAAGATTTTG 150  
CAGATTTACA ATTTGGGTTT TTGTCTGGAG TTGCTTCGGT TTGAAGCCCC 200  
CT 202

20

## (2) INFORMATION FOR SEQ ID :170:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :170:

35

TCAGGGAACC AAAAACTGG CTTGCTTGGC ACCCAGGGAC AGTAGCTGTT 50  
TGGCTCTCCA CCCAATTAAA AAAACAAATC CCTGCCCTTT CCCCCACCCC 100  
ACTAGCTAAG CAAGAGCAGA GCTCTGATGA AGAGCCAGTG CCGGGTGCCT 150  
GGTGCCCAAG GCTGTAAA 168

40

## (2) INFORMATION FOR SEQ ID :171:

102

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :171:

10

AGAAGTCAAC TAAAGCTCA ATGCATCAAT TTATAANGCC TCANAGATCA 50

GCAATTTATG ACACTTACAT TTACAGTCCA CCTTTACTAA CCAGGCAAAC 100

15 TTCCCGAAAT GATCAGGACT GATTCATCTC CTGAAATTNN CNGT 144

## (2) INFORMATION FOR SEQ ID :172:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 91 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :172:

ACCCACAGNN NNNACCTAGA GGCCAGCGC CCAGAGAGGC ACGTAGAAAT 50

30

GGGGACAGCA CGTTTATAGA CCACCAGAAA TTGAAGAGGA A 91

## (2) INFORMATION FOR SEQ ID :173:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

103

## (xi) SEQUENCE DESCRIPTION: SEQ ID :173:

|    |  |     |
|----|--|-----|
|    | GATTTTTTAA TGGGTNGCCT CTTTtagctt GGAATATTAC GTTACTTTA  | 50  |
| 5  | ATCCAAGTCT AGGCCTTTTA AAGGGTCCTT AAAATTAAAG TTCAGAATGT | 100 |
|    | GAATCCCTTT GACATCTATT ACAGGTTATA GGACCTTTTT GGTGTGATTA | 150 |
|    | CGGTTTTCAA TACGATTGTA TAAATGAAGT TAACTGGCA GAAGTAAAA   | 200 |
| 10 | TGGA   | 204 |

## (2) INFORMATION FOR SEQ ID :174:

|    |                               |
|----|-------------------------------|
| 15 | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 241 base pairs    |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |
|    | (D) TOPOLOGY: linear          |
| 20 |                               |

## (xi) SEQUENCE DESCRIPTION: SEQ ID :174:

|    |  |     |
|----|--|-----|
| 25 | GTAAATTTCa CTACATCTTT TNNTNGACT TTCATGCATT TCTCATACAT  | 50  |
|    | TNNTNNCNGA TGCTTGACTT TATTGCTTCC TAGCAATAAT CTGCATTTAA | 100 |
|    | ACGAAAGGCG GTTCAATTCA TCAACTTGAA ATGACTATTT ATTTTnAGG  | 150 |
| 30 | ATTTTTTAGG GGAAGAGTAC CCATTTCGTT TATAAAAACA GATGACAAAT | 200 |
|    | TTCTTAAAGA AACAGAAGCA CAATACTTTC GAAATACAAC G          | 241 |

## 35 (2) INFORMATION FOR SEQ ID :175:

|    |                               |
|----|-------------------------------|
|    | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 211 base pairs    |
|    | (B) TYPE: nucleic acid        |
| 40 | (C) STRANDEDNESS: double      |
|    | (D) TOPOLOGY: linear          |

## (xi) SEQUENCE DESCRIPTION: SEQ ID :175:

5 GGTGGGCTCN NNNANNANNG TTCTACACTG TGGTATAAAC TTGTCGTGGT 50  
TCTCGTGATA GAAAACAGAC ACTGACCTTG GGTATAGTGG GCCTATAAAT 100  
AACAAACCCT TGGGTACTCC TGAATAGGGG CAGGGCCCCC TGGGCCTCCC 150  
10 TTACAGGTTT CTTCAGGGAA ATGGTCCCTG GGATAATTCT TTAGGGCCCT 200  
TTGGCCCTTT T 211

## (2) INFORMATION FOR SEQ ID :176:

15

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :176:

25

AAAATAAGAA TAAACATCCA TAATAGTNAT AGATANATCC NTTTATTTAG 50  
NACATCAGCA ACGACTGCTT CACACCAAAT CCCTTCCTCT GNGAATGATN 100  
30 TATATAACTC TAGTACTGCT TTCCATGAAG AACCTTGCAA ATTGATTGAA 150  
AGTCCAGGAT NNCTCGCTAA TCCTCCACCA TAAGATTCT GACCTATGAT 200  
AACTCCAAGG TGGCAAACAG AGAAATCAAC TTCCTTATAA ANAAATCCNA 250  
35 AT 252

## (2) INFORMATION FOR SEQ ID :177:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 279 base pairs  
(B) TYPE: nucleic acid

105

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :177:

GCGGGCGACT TTCCATCCCT CGAACCAAGG CATGTTAGCA CTTGNCTCCA 50

10 GCATGTTGTC ACCATTCCAA CCAGAAATAG CACAAATGCT ACTGCGCGAG 100

TTGCAGCCAA TCTTCTCAAA GCAAACCGAC TTCCTAACAA CTNCTACAT 150

CTGGCTCGCT GCAGGCGACT CAATGAAATC CATCTTTAAC ACCACAATCA 200

15

TTGTTNACA CCCAGTGTGC AAGCCAGGAG GGCATGTTCT GAGTCTNTCC 250

ATCTGAAGAT ACCAGCTTCA AATACTAAT 279

20 (2) INFORMATION FOR SEQ ID :178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 157 base pairs

(B) TYPE: nucleic acid

25 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :178:

TATGCCCTGA AATGAAACCT CTAAGTTGA CAAAATACCC ACAAAAACAG 50

ACCTTCCTNG TTAACACTTT ATAAGAAGGT GTGACATTTG GTGGGTGGTC 100

35

GTTCTCAATT TATAAANAA TAAATGACTT TAAAGGAGAA ATAAATTTAT 150

GTCAGGA 157

40 (2) INFORMATION FOR SEQ ID :179:

(i) SEQUENCE CHARACTERISTICS:

106

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :179:

10 GATAATGCAA CTTTGGACAG GAAAGCGCGA TTTTACTAT

39

(2) INFORMATION FOR SEQ ID :180:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 157 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :180:

25 GCAAATCAA ACTACGGACG CACTCACAAT CGCTCATAAT CCTCTCTAAG 50

GACTTAAACT CTACTACACT AATACTTTTT GATGACTTCT AACAGCCTC 100

GCTAACCTCC CTTACCCCCC ACTATTAACA CGGGAGAACT CTCTGTCTAG 150

30 TACCACA 157

(2) INFORMATION FOR SEQ ID :181:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :181:



107

CCATCCAGGC CAAATAAGCN CCGGCTATGC CCNTGTATTG GATTGCCACA 50  
CGNCTCACAT TGCATGCAAT TTGCTGAGCT GAAGGAAAAG ATTGATCNCC 100  
5 ATTCTGGTAA AACTGGAAG ATGACCCTAA ATTTTGAAGT TGATGATGTG 150  
CCATGTGATA TGGTTCTGAC AAACCCATGT GCGTTGAGAG CTTT 195

(2) INFORMATION FOR SEQ ID :182:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 146 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :182:

20

CATGGTCTTA ACCAGTGTCA GATGGAATCA GTGGATAAAT CCCCAGGTTT 50  
GTTTGTCTT CAAATGGGAC AATTGAGGA ATGCTTTAGG CAGAGGACTC 100  
25 AGATGACAGA GCGCCAACCA CCCACAATAG AACCTGCTC ATCACA 146

(2) INFORMATION FOR SEQ ID :183:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 50 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :183:

TAGAGGAATA GGGNNNGNGA CGCCCNAGT TGTAGGGACG GACGGAGGAC 50  
40

(2) INFORMATION FOR SEQ ID :184:

108

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :184:

10

ACGNTTACGG TCACTGATAG TTGATGTGCN NCTGAAACCC ACATCCGATC 50  
AATCTCCTCA TAGAGCTTCT TCTTCACCTG AGGATTGCGC AACAGGAAGG 100  
CCAGGATCCA TTTACCACAG AGGCGGGATC TCCACGCCAA CCCCAAAGAT 150  
GTCCCCTATG ACGACGAGAA TGTGATTATC TGAAAGCAAC TTGATCTTGA 200  
TCTGGGCCAG CATGCCTCAT CTGATTCATC TCGCTTCCAT CAATGNGT 248

20

## (2) INFORMATION FOR SEQ ID :185:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :185:

AATGATGAGT AAAAGATTCA ACAACTCACA GCCCTGGGGG CACTCAGGCT 50  
ACTGCTAAGG CCTGAGAGTT TTGCAAAAAT GCGCAGAGAA ACACCCTTTG 100  
AACGTGGCTT TCT 113

35

## (2) INFORMATION FOR SEQ ID :186:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 base pairs

109

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :186:

GGGCCCCCTG ATCAATTCTT TGGATGCTTT TCAAATTTC CAGGATCCCG 50  
10 ATGTCGTCAT ACACTCCGAA CATGACCCTT TTTTCTTCCA ACGATCAACC 100  
ACTNCGNGGG ACGGGAGAGT GAGCCTTATA CCGATCAATC TGCACACC 148

15 (2) INFORMATION FOR SEQ ID :187:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :187:

TCCTTACTGT AAGAGCCATT TAAACGATTA AAATCCCACT NGCCATACCG 50  
TAAGATGATA GGACCAACCA TACCTACCGA TCAAAAATTT ATCAATCCAA 100  
30 GCCAACTACA CTCCCACTGC TAAAAGATG AAAGGACCAA TCAAAGATTT 150  
AATTAACTA AAGGGAAAGA ATCAGAGACA GAGAATGAAG AAAGAAATTC 200  
35 TAAGTTGCGA CGGACAAACC AGAACAGACA ATGAAGCCTT TCAACTGC 248

(2) INFORMATION FOR SEQ ID :188:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 146 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

110

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :188:

TATGAAGAAG TGCAGCACTG GCCAACACCA GGGTTTACTG AATCATTTC 50  
GTTTAATACA TAAGTGTCCTA ATAATAATGT CAACCCTCCC TCGCCACAGC 100  
CAATAATTTC TCCTCACTGA GTTGGCAACA AGTGACTGCT GTGACT 146

(2) INFORMATION FOR SEQ ID :189:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 81 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :189:

25 ATTTACCACA AGGGACGATT TCCACACCAA CCCCAGAAAT GTCCCCTATG 50  
ACGACGAAAT GTGTATTGA AACAGCTCTG A 81

(2) INFORMATION FOR SEQ ID :190:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :190:

40

AAGTACAGCA TCCTGCTGCA AAAATGATTG TAATGNCTTC TCATATGCAA 50

111

GAGCAAGAAT TGAAGATGCA CAAACTTCGT TCTGAATTTG TGAGCTTCCT 100

GGATCAACTG AAGAACTTCT GAGGATTGAC CTGTCA 136

5 (2) INFORMATION FOR SEQ ID :191:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 152 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :191:

AGGATTTAAG ATGGGGACAG ACTGCTGAAA ATCGGCTGA CTGGAAGGAA 50

ATGGGGCATA CGAGTAATAT GTACATATCA AACAAATCAAT TGCCTCCTGA 100

20 AATCAAAAAA TCAAATGGTG AAATGGAGCC TCCTTGATAG TTAGGCCAA 150

CA 152

25 (2) INFORMATION FOR SEQ ID :192:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :192:

TAAGCGAGGN NGTCTTTGAT TCGCTAGTAA GGTAAAGACG ATTTTATAGA 50

ATNAAGGTGA TTCCT 65

40

(2) INFORMATION FOR SEQ ID :193:

112

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :193:

10

AGGACCCAAA CTACCTTATT GCATTGAAG TTTTACTTAT NCTATTATAA 50  
TCTAAGAGCC CACCCAACAA GGCCTACAC ATAGATGCTC AACTCTATA 100  
GGCTGCCTGA TCCTGGACCA CCTGGGGCCC TGATTATGAT CTCCACGGGG 150  
CTGTCAATGA CTAGGGAAAG CTTTTTAAGA CCCAGCGATC ATGCAATGGC 200  
TCAACCATGG CGAATCAAAG TTAGCATAAT GTCCCAGCAA ACAATGTTA 249

20

## (2) INFORMATION FOR SEQ ID :194:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :194:

GGAAAGGGTG CCTCATCCCA GCAACCTATC CTTGTGGGNG ATGATCACTG 50  
TGCTGCTTGC NNCTCATGGC AGAGCATTC A TGCCACGATT TAGGTGAATC 100  
GCTGCATATG TGA CTGTCAT GAGATCCTAC TAGATGATCC TGA CTAGAAT 150  
GATAATTAAA AGTATTTACT TCGAAGCACC ATTTGAATGN TCAT 194

40

## (2) INFORMATION FOR SEQ ID :195:

113

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :195:

10

GTGATTTTAG TTTAAGGATA AGAAGCCACT ATATCAACGT CGGGGGGGTA 50

TTTAAGTCAC ACACATAGTT AACAAACNCNC GTNGCGTGCA ATAAATACCA 100

15

CATCCTTTNA TATGNNCNGN A 121

## (2) INFORMATION FOR SEQ ID :196:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :196:

GGGCTTCNNN NNNNNNCATG TGCACTTAGA ACCGTTACTA ACCGAAACAC 50

30

CATTTGCTTG TCAACAATGT ACCCTTGACA GCAGGGAGAA ACTTCTTTAT 100

AGTCTCTGCT TCAGACAAGA TTTACNGCTT TCTCCAAGGC CAGAGGCAAA 150

35

TTGTGACCAC AAGTCTTGTT TCTTG 175

## (2) INFORMATION FOR SEQ ID :197:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 273 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

114

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :197:

ACTGGCAACT TCTATGTACC TGCAGAACCC AAATTGACAT TTGTCATCAG 50  
AATCAGAGGT ATCAATGAAA TGAGCCCCAA GGTTCGAAAG CTCGCAACTT 100  
10 CTTACCTTC ATCAAATCTT CAACGACCTT CGCAACTCAA CAAGCTTCTT 150  
ACAGTGAGGA TTGCAGAGCC TATATAGCTG ATACCCCAAT CTGAATCATA 200  
15 AATGACTAAT CTACAAGCNT GTTATGCAAA ATAAATAAGA AACGACTTGC 250  
TTACAGATGC NTTTTAATTG TGG 273

20 (2) INFORMATION FOR SEQ ID :198:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 56 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :198:

GATTCCCCAA TAAGCAGACA CCTTGAACCA GCCTGGGGTG AGCGAAAGAT 50  
GNTATA 56

35 (2) INFORMATION FOR SEQ ID :199:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 132 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



115

## (xi) SEQUENCE DESCRIPTION: SEQ ID :199:

5 GGACGCTGNN NNNNNNATCC TGCAATGCAC AGCACAGACC CCACCACAGG 50  
GGTTTTATCC AGCCCAAATG TCAACAGTGT CAAGTTTAAG CAACTCTTAC 100  
CGAGTGGGAC TCAATTCCCN AGTTGTATGG AA 132

## 10 (2) INFORMATION FOR SEQ ID :200:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 284 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 20 (xi) SEQUENCE DESCRIPTION: SEQ ID :200:

AAACTTTTTN GCACTTACAC AGACGAGACT TCACTGCNTG AGGATCATAC 50  
GACATTTCAA TCGNACACAA ANTTAAAAAA TAAAACAAAT TTAAAAAAC 100  
25 CATNTTGAAT TTCCTTAAAA TTATTCCAAT ACTTTCCAAC TTAAATTCA 150  
GAACAAATCC TCCTAGAGAC TATCAATACC AATATCTTCA CATTGCTCAG 200  
30 CTGNTACATA CGNCCCACCA GTTCACTAAT AATGACACAA CACTACATGN 250  
TCAAATCTTA TCTNNNATAG CACAGTAACA AAGT 284

## (2) INFORMATION FOR SEQ ID :201:

35

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

116

## (xi) SEQUENCE DESCRIPTION: SEQ ID :201:

5 CCTGACACCA ATTTGCCCCA CATGTATGCG GGAAGAGGCC TGAGACTAGA 50  
AGTCGTTGCC CTGTCCATCT CCCGGCCACA GGCTTCATTC CCAGATTNT 100  
CTTGNT 106

## (2) INFORMATION FOR SEQ ID :202:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :202:

20

CTTTGAAAA CAAACATTTN TTATTACTGA AATAGCAAAA ATCATTCTAC 50  
ACTCCTCCTA AGCATGTTCA ATTAGCATAC ATTCCAACAA TGCATGAAAA 100  
25 AATTNCTAGC CAGAGGCATT TAAGTGATTT CTTCTAAGT GTTTGCTAAT 150  
TCAATGCCAA GAACTATGAT GTTTATCNTT CTGATGGACA AATCAAGAAA 200  
CAAAACAGAT ATAATACCAA GGGTAAAGCT GATATGACCC ACAACATTGT 250  
30 CATTACTCTA ACTGTTAATC 270

## (2) INFORMATION FOR SEQ ID :203:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

117

## (xi) SEQUENCE DESCRIPTION: SEQ ID :203:

AACTAAGGCA CATTGCCCTT TTTGACCTTT CTNNNGNACT ATTGAAATCA 50  
5 AGCTTATTGA TTAGGTGATA TTTTATAAC AATTGAAAGG GCAATATCAA 100  
ATAATGACAT ATGAGAATTT TTTATTACAT ATTAAACTG ATTTTACTT 150  
TACAAAANNG NAATTGCAA TTA 173

10

## (2) INFORMATION FOR SEQ ID :204:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 164 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :204:

CTGCTTCACC ATCCTGGCGT CTACCAGCCT GGTGNGGCTG GGTACTGTGN 50  
25 ATCGTCTTCC TCAACAAATG CGAGACCTGC CAACCTGCAC TACACCACAT 100  
CCGCNCAAGA AGAAGAACCT GCTGCTTCAT ACAACACGGG GAGGCCCTGT 150  
CATTACATT ANTT 164

30

## (2) INFORMATION FOR SEQ ID :205:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :205:

118

GACCGCCCAN NNNCATCCAA AACTTCTAGG CACAATCTAT ACTGCTGCTG 50

AAGAAATTGA AGCAGTTGGG GGAAAGGCCT TGCCATTGAN TTTTGATNT 99

5 (2) INFORMATION FOR SEQ ID :206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :206:

GTACCTTGGG NNNNNNANNG GGAATGAGGT TCTACCACTC TGGAAAATTC 50

ATGCCTGTCA NTNTAANTNC AGGTGCCAGT TNNCNNTAGG TCGCCAAAGT 100

20 TGGGGTTAGN TGTTCNAA 118

(2) INFORMATION FOR SEQ ID :207:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :207:

35 CACACTANCG ACCAACACTT AAAAGNCTNC TCACACAAGN ATCTTTTTAA 50

TAAAAATACC TCTTTCNTAA CTCCACTTA ACTCCCTAAA ACCCATGTCTG 100

AAGCCCCCAT CCTGGTCAAT AGTACTTGCC CAGTACTTTT AAAACTAGGC 150

40 GCTATGCATA ATACCCTCAC 170

119

## (2) INFORMATION FOR SEQ ID :208:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :208:

TTCAATGAAA TGCTTGATA CAATGATATA ACAAAGAAAC CCTAAGACAA 50  
CGAGAACTTC AACTAAGTGC ACTCATGCAG AATCTCTGCG GGGAGAATTT 100  
TTTCTCGGGG AAGTAACCCT GCCTTTGAA 129

## (2) INFORMATION FOR SEQ ID :209:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :209:

CTTGGCGTCA TTTTCTGTAC TTCTGACAGT GCCCTCAGAG TCTGCAGGTG 50  
GATCCTTTTT TGCAATGGCAT TAATTATATG AGCAGCCTCC TTCTGACAAT 100  
CCAAATTTTG GCTCCAGAGT CATTTCTGAA NNTCTACACT TANGGNCTTN 150  
AGCNTGCTCA TTCAAGGTNA AGGGCAGTTT TNAAAAATAT 190

## (2) INFORMATION FOR SEQ ID :210:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs

120

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :210:

TCATTGAGTC ATCCTTTTTG CCTGCTGCTG TAAGGTTTTT TTCCTTCTAG 50  
10 TAACTGTATG ATCCAGAGCG ACCCAGCAAG GACTCAATCG ATCACCAACT 100  
GATGCAGAAC TGTTTCATAT CTAGAAATG 129

15 (2) INFORMATION FOR SEQ ID :211:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :211:

CTGTAAGGTT TTCTTTCTTC TAAGTAACTG TATGATCCAG AGCGACCCAG 50  
CAAGGAATCA TATCGATCAC CAGCTGATGT AGAACTGGTT TCANATCTAG 100  
30 AAATGGAANC NNNNGGTTTN TTCCTTAATG GACCCCCCN GGGGCNGAAT 150  
GG 152

35 (2) INFORMATION FOR SEQ ID :212:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 186 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

121

## (xi) SEQUENCE DESCRIPTION: SEQ ID :212:

5 CTTAACCCTT TGGAAGGNTT GACTGTGTGA CCCGCAGCAA ATAATTCATG 50  
TCGAAAGATG AAAACAATA AGTTCATAAC CCCCTGCCCCG CCATTGACCT 100  
CCCTTTNAAA ANCGAGACCA AGACTCCATC ACTGGTTTCG AATTACATC 150  
10 NAACTGCTAA GATTGATACA TTNCAAGTCT GCAAAT 186

## (2) INFORMATION FOR SEQ ID :213:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :213:

25 CTTAAATGCC TGTGTGATA TCTTCTTTAA ACCTGGAGAG ATTGAATCAA 50  
CCTTTCTCTA AAATTCCTTT CCTTTGCCTC CTCCTCTAAC TTTTCCTCCT 100  
TTCNCGCTTT TCCTCAGGCT TTGNTTTTCC TCATGCTTTG CTTCACTCTA 150  
30 TT 152

## (2) INFORMATION FOR SEQ ID :214:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 290 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :214:

122

TCTTCAGGAG AAGGGGCACC ACTGCTTTAA AAAACAATAC TCCNTTATAG 50  
ACTTGAACAT TTGCAGACAT TATGATCTTG CTTCCAACTC CCACCGTATG 100  
5 TCCAGCAAAC TCTCGCATGT GGCCACTAGG AGGAATGCGC AAGAATGTTC 150  
ATATTACATA TTTATAACAT TAATAACTGG AAAAAGTGAA ATGCATGTCT 200  
GTTACAGGAA AATAGGCGAA TAATCAGATA TATATATCTA NNNCCGGGAT 250  
10 ATTATTCAAT AGTGGAAATG ATGACTACAG CTATACCTCA 290

(2) INFORMATION FOR SEQ ID :215:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 273 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :215:

25 GTTTCCTCCA GTACATCCAA GTTTAAATTT ATTAGCGAAA TGGTCCATGT 50  
TTTTTCAATT ACTGCTGACA CGATTCTAAG CTAAGTGAAG GGGAAGATCT 100  
GAGAGCATGC TGTCTGGACT GTTGATGCAT ATTCATGATG TAACAGGTCC 150  
30 TGGGCCTCAC TTTACCCCAT TCGTAAAATG GGGATAATGT CACCTGCCTC 200  
TTACCTACCT CAGAGGGATT TCGAAGCAA ACTGTTAATC TTCGAAAACG 250  
35 ACCATTTACT TTAGGATAT CAA 273

(2) INFORMATION FOR SEQ ID :216:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double



123

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :216:

ATCTACGGCT AGGGAGAAAC AATGTTCCCTA CATATTATGG GTAGTGAGAA 50  
CATTATCTGT ATAACAGGGA ACTGTGATTA TTTAAAATTA TGCAGAACTT 100  
10 ATTCATCTG TGCTTTAG 118

(2) INFORMATION FOR SEQ ID :217:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :217:

25 GAGGCTGGTG GCGAGGGAGT TGTGGAGGAT AACAGAAGA AAACAAGTCT 50  
ATCACTAATG ACTTATTTTA CTTAGTTTCC ATTCACGAAA CCCTTTTAAA 100  
TACAAGGCAA CATTTTCACA GCTGAAAAAT TACAACTAAA NGNNNTGATT 150  
30 TACCACCAA AGCAATAGAT GTAGTTATGT ATAATCTATA GATAATA 197

(2) INFORMATION FOR SEQ ID :218:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

124

## (xi) SEQUENCE DESCRIPTION: SEQ ID :218:

CTCGCGAGCA CTCGTCCGAG AGGTCCCAT A C N N N N N N N C C C A A G C C C C T C 50  
5 A A G G G C C T T T G C C A A T C T N G T C A T T T T A T G C C A A G T C C T C T A A A C G C A C 100  
T C A G G G G T A T C T A C A T C G C A C T T G T A C A G A A T A C A A G A T C T T A T C C T C C 150  
T A T T T T A G G C T N C N A G G T C A A A T A A A 177

10

## (2) INFORMATION FOR SEQ ID :219:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 118 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :219:

G A A A T G A A A A A G A G A G C A T T A T T G G A A G A A T G A A A A T A C A T C T C A G A A A 50  
25 G A A A C C T A N T A G T T C A A C A A A T T A A A A G A A A G A A A G A A A A A A A G C A A A A G 100  
T N G G T N T C A G G G C T G G A C 118

## (2) INFORMATION FOR SEQ ID :220:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :220:

G A G A G C C C A G C A C G T C A T C C C T G A T C T G A G T C T A C T G A A C A C C T G T T T T 50

125

ATGGACTACA CTGTCTTTTC CTTTGAATCC CCACTTCTCC TGGAAGTGA 100  
CTTGACCAC CAGGAACATC GTAAGACACA ACCCAATACA CTCACCGCAT 150  
5 TCAGACAACT GTCCAGACAC TGCCCTGACA CCACAGGGNC CCCTTTACAN 200  
NGGTTGGNGG AAATATNNTT TAATCTCAGG CCA 233

## (2) INFORMATION FOR SEQ ID :221:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :221:

20

GCACACAGAT ACCATCCCAC CTTGCTTTNT GACAGGCCAG CCACACAATA 50  
ACCCTTTCCC TACTCACTAA AGCATCCCTA GGACACCAAC AATGAGGACA 100  
25 GGCAGACTTA CCCCCGCCAT CTAGAGAGAA TGTCGTTATT ACCCATAAAA 150  
CTCGACCACC CCCATATNCA CTNTTGGGTA AAAACAAACG CTTAAACCTG 200  
TGAGCCTGCC ATTCCTTTTT ACGTGTTAAT CAATT 235

30

## (2) INFORMATION FOR SEQ ID :222:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :222:

126

GCCAATNNNN NGGCGCGAGG GNNAGAGAGA ATGGCAAACA GGGACCCGGG 50

CCTTAGGAAT TGANTGAGGA CTAAATTTC CCCNGAGGGA GAGNAGTGA 100

5 G 101

(2) INFORMATION FOR SEQ ID :223:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 271 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :223:

ACGGTGACTT TCCATCCCTT GAACCAAGGC ATGTTAGCCT TGGCTCCAGC 50

20 ATGTCGTCAC CATTCCAACC AGAAATTGNC ACAAATGCTA CTGGTCGGGT 100

TGACCAATTT TCTTAATGAA GTGCTGACTT CCTTAACAAT TTNTTATATT 150

25 TNTTCGACTG TAGGGCGCTC ATGAATCCAT TTCGTTAACA CCGACAATTA 200

ATTGTTTCAC ACCCAGTGTG CAAGCCAGAA GGGCATGCTC TGGGTCTNCC 250

CATTCTTGAG ATACCAGCTT C 271

30

(2) INFORMATION FOR SEQ ID :224:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :224:

127

AGTATTATTT ACTNGGTCAT CTGGGAACCT TAATGTGATT TATTTTGACA 50  
ATTACTGTGG CACATGTTTA ATCTGCAGCT CCTGGCGACT ACTGTGCTTA 100  
5 T 101

## (2) INFORMATION FOR SEQ ID :225:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 141 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :225:

TTCATTCCCT CCAGTGCNCG NNCATGCGAC ATATACAGGN NNTGTACCGT 50  
20 AGGCGCTANT GTGTGGTACT CTGCCACGNN ANACCNCNNC TCGTCTTGAA 100  
GACCCTGTTA ANTTTGGTGA AAATAACTTT CCANATTTC A 141

## 25 (2) INFORMATION FOR SEQ ID :226:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :226:

ATTTTCTTAT ACTCCTCCCA CAGATGAGTT CACAAATACA AAAANTGGTG 50  
TACATTTATA CTCAAGNACA AATCTCCAAC AGCCAAGTAA TTATAGTTTG 100  
40 TTCTGTTATG TGCAAAGTAG ATTATTCAT ATTTACTTGG TATGGAAAGC 150

128

AGAGTACAGG CTCAATGGAC AATAATCATT AAACACACAT TATNTTTAAG 200

AAAANGCTGT TNNAAAAA 218

5 (2) INFORMATION FOR SEQ ID :227:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 209 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :227:

GAAAACTTTA TTGTGCCACA CCAGGATTAC CGAACAGAAN NACNNGGTGG 50

TGAGAAGTTG GTATTNATAG CACCTTATTT ACATGATGGA CTTGAGGAGG 100

20 CAGTTAATCC TATGGTTGTG TATCACAACC TTTTATTAGC AATGCCATCT 150

TCGTCTTGCC TCCNCCCTAC TTGAATATCC CTTACGGTCA ACANCCCNCG 200

25 GGGTTGGGC 209

(2) INFORMATION FOR SEQ ID :228:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :228:

TTTNNCAANC CAAATGGTTA TTTATTCTAA AACTGGAAGC TACTTTGCCT 50

40 ANCATTTTCG CCAGAATGGT GTAATGNNNA CAGGGGAGGA AAAAAGTTAC 100

129

AGATGTAAAC AATGACACAG TTACATTTTT TTTTAAATG GTAAAACCCC 150

TTTTTACTGG NCNTTCCAGA ANCTTACAG 179

5 (2) INFORMATION FOR SEQ ID :229:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :229:

AGTTTAATCT CANNNNNNNA TGTCACAAGT TATTGTAGCA GTGAAACAAT 50

GAGGGCATACT ACTATATNGA AAAAAAACC TCCTCCCTNA TTCTCAGGCC 100

20 AACCACAGGC TTCTGCCCTG CAAAGATCAC CAATGTCAAT AGTTTGGTAA 150

TACACCATCA TAAAGGNTCC TAAATTCATC TCTA 184

25 (2) INFORMATION FOR SEQ ID :230:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 140 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :230:

GAGACAGATG TANNNAAAGT TCAGAATACA ACAGTTAAGA CTCAGTTTTTC 50

TTTTTAGGTT TAGAATTTGA GAGCAAGTAT TGNTATGGTG AGCTGTTTTA 100

40 GTGCAAACAT TGTGAGTAT GTTGTCAAAC GTCTAAAAAA 140

130

## (2) INFORMATION FOR SEQ ID :231:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :231:

CGGAGACTTG TCCAGAGAGT TGTCTCTTNT NNGTTGGGGG CCGTCCCGCT 50  
15 CCTAAGGCAG GAAGATGGTG GCNNNTNNG ACGAAAAAGT CGCTGGNGNN 100  
NATNAANTNT AGGCTCNAAN TNNTTATGAA AANTGGGAAG TAANTNNTCG 150  
GGGGTAAAAG NAANATNNGA ANATGGAT 178

20

## (2) INFORMATION FOR SEQ ID :232:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :232:

GAGCCAACGC CACNNNNNAG NTGAACCACA CTCACGAAAA AAACNCNTAC 50  
35 CGTCGTCNTA ATACNNANTC TTCCCATACA AAAATCGTCC NTNTAAATNT 100  
NNTAAACCAA TTCACAGCCC ACAGAACNAA TCAGTAATTT TATANCTCN 150  
NCGAAACCAC ACTTATCCCC ACCTTGGTCT ATTCATNACC CGGATNGAGG 200  
40 GCAACCANGG 210



131

## (2) INFORMATION FOR SEQ ID :233:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :233:

|    |  |     |
|----|--|-----|
| 5  | ACTGTGCGAG TAGCTTNAAA ANNNNNNNNN NNACTCAGTT TNATTATAC  | 50  |
| 15 | AAAAAGAAAG GGGTGTGNAG TCCATGGTGT TGTACAGTNT NTAATTAGNC | 100 |
|    | CANNACGAGA AAANANATNN NNNTNNNAAA NNNTGAATTA TGGGGTNAGG | 150 |
| 20 | ACTNTCTNAC NTTCAAACNA NTATTNCAGG TAAAAACAT CACAGTGCGA  | 200 |
|    | AGAAAGNNAN CNCANNTAGA GCANGAAGAC ATCAAAAGCC AGCCGGG    | 247 |

## (2) INFORMATION FOR SEQ ID :234:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :234:

|    |  |     |
|----|--|-----|
| 35 | AAACACCAAA NAAANNNNNC NAGCAANAAA GTGGAAGACT AACCAAGATT | 50  |
|    | GTGGACATTG GAATGTTTAC TGTATTCTG TGTAGAAAA CAACTNACAA   | 100 |
| 40 | AAAAGAAAA TGGNCAACAA AATTGTTTCC CGGCNAGGCT GNAGGAAACC  | 150 |
|    | NGGGGGAAAN TGCCNGGGC                                   | 169 |

132

## (2) INFORMATION FOR SEQ ID :235:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :235:

GCANCAACANA AAGGAGACGN NANAGCAACG CAGAGATAGC CATCCAGATA 50  
15 G 51

## (2) INFORMATION FOR SEQ ID :236:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :236:

CAAGTGTAAG TGCTTGCACC TCTCTNCCTC CCCGANTGAA CTCTCTGATC 50  
30 TCAAACITTT TTAGGAAAGC CAGATTAAAA GCAGACGTAC CTAAATNCAA 100  
A 101

## 35 (2) INFORMATION FOR SEQ ID :237:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 156 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

133

## (xi) SEQUENCE DESCRIPTION: SEQ ID :237:

5 CATTATAAAA CAGCCTAACT TCCCTTATGC CATATGATTG CCTTAAAAAG 50  
ACCAGATCTC AAGGAAAAGA TCATCAAAGA GCAGAGATCT TGAAGCGGCA 100  
CAGTTTTCCA GCAGTTTTCG TATTNTTTT TATTACGAA TGCCATACTC 150  
10 TGTTTT 156

## (2) INFORMATION FOR SEQ ID :238:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 148 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :238:

GCAGNCTAAT TGTGAATCTA AGAACTACT CATAGACATC CCACCCTAAT 50  
25 GATTTTACCT NNAACNTTTC TCCTTCATCA TAGAACCCTA GCAACATCCA 100  
CCTCCTGTAG CACGAAACGA ATCAACAAC CCCCTGGATA ACCTCTCA 148

## 30 (2) INFORMATION FOR SEQ ID :239:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 258 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :239:

GAGTTTAAAC TTAATCACCT CTTTAAAAGA CCTGTCTCCA AATACAGTTA 50

134

AATTTGAGGT ATTGAGGGTT AGGACTTCAA CATGTGAGTT TGGGAAGGGA 100  
AGCACAAAAT CAGCCCCTAC CATGGTATAT TTATCATTGA TACATTACTA 150  
5 TCAACTAAGC TCAAGATTTT ATTCAGATTT GACTAGTTTT TCCACTAAGG 200  
CCCTTTTCT TTTCTAGGNT CCCACAGAGG ATACATTACA TTTACTTACA 250  
TCTTCTCT 258

10

(2) INFORMATION FOR SEQ ID :240:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :240:

GAGCATTATT TGATGCAGAA GTTGAAAAAC AATAGACTCA AGAAAGAAAA 50  
25 CAAACCACTG ATTCCCCTTC CTCAGATACT GGGACTAACA GCTTCACCTG 100  
GTGTTGGAGG GGCCACGGAG CAAGCCAAAG CTGAAGAACA CATTTTAAAA 150  
CTATGTGCCA ATCTTGATGC ATTTACTATT AAAACTGTTA AAGAAAACCT 200  
30 TGATCAACTG AAAAACCAAA TACAGGAGCC ATGCAAGAAG TTTGCCATTG 250  
CAGNTGCAAC CAGNGGAGNT CCTTTNAAGN GNAACTTCTN GNATAATNNC 300  
35 AAGGGTNAAC NTNTTTNNAA ANNNGCCNAA NCNNGATTTT GNACNCCCTT 350  
TNNCATTGGC ATTNANTGAA AAAAGTT 377

40

(2) INFORMATION FOR SEQ ID :241:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs

135

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :241:

GGNGCACTGN TCCGAGAGCT TTTTNNCTG AAGAATAGCA TCTTTAATGA 50  
GTGTNCTAAT CCTTGTATC TGAAGTTTG AAATATATT CCCAGGGTCA 100  
GAACAATACA GAGA 114

15 (2) INFORMATION FOR SEQ ID :242:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :242:

CTCAAAATNC TGTGACAAAT TTNNNNGGTC AAGTTGTNN CCATTAAAAA 50  
GTACCTGATT TTCAAAAACC TAATAACCTT AAAACCNCCC CACGNAAAAA 100  
AAAAAANCNA AAGNGGGCCC CC 122

30

(2) INFORMATION FOR SEQ ID :243:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 171 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

136

## (xi) SEQUENCE DESCRIPTION: SEQ ID :243:

GAGAATGGGA AGCCTCATTT TGGGGACAAG AACCTGTACA AGGATTTGTG 50  
5 ATGAACTTTT CCAATGGGGA AATTATAGAC ATCTTCAAGC CAGTGCGCAC 100  
NTATGATATG CCTCATGATA TTNTGTCATC TGAAGATGGG ACTNTGTACA 150  
TTGGNGATGC TCATCCAAAC C 171

10

## (2) INFORMATION FOR SEQ ID :244:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :244:

AACTTTACTG TCAGATAATA AAATTAGGGC TTTCTCTTAA AGGGCTTCTT 50  
25 TAAGAGAAAT ACAGAGTGTT TGGTATNTGA GAGAAAAAAA GTTAAACAG 100  
GACTTTCAAC TTAATCCAGA CTTCTAACA GTGTTTACAT GTGAGGGAAA 150  
CTCCTTTAAG TAATGCGTAG TGTATTATTT TTACCATCAT TGGNGACAAA 200  
30 AAAAAACAAA ACATAAACAT CTNANGTGAA ATATA 235

35

## (2) INFORMATION FOR SEQ ID :245:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

137

## (xi) SEQUENCE DESCRIPTION: SEQ ID :245:

|    |  |     |
|----|--|-----|
|    | GGCCTAGCCT GCCATACCCT TACGAGCAGG CTCAGTGATT AGACTTTGAG | 50  |
| 5  | TCTAAGTTAA AAACGCCCTG CCCCCTTCTC GCAGGCCACC TACACCGTNN | 100 |
|    | TTTTATCGAT TTGATAAAAC CACCAGCCTA CTCATCAAGN NGCACCCTGC | 150 |
|    | NTNTACNTCT AACCNAAACA TNACNGCGGC CACCTACTCA TGCCCTANTG | 200 |
| 10 | CAGCNCACCC T   | 211 |

## (2) INFORMATION FOR SEQ ID :246:

|    |                               |
|----|-------------------------------|
| 15 | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 194 base pairs    |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |
|    | (D) TOPOLOGY: linear          |
| 20 |                               |

## (xi) SEQUENCE DESCRIPTION: SEQ ID :246:

|    |  |     |
|----|--|-----|
| 25 | GGCTGAGAAT CCTTGAGCTT ACCATTGAT ATTTCTATAT TATTTAAGAA  | 50  |
|    | AAGTCAAAAG ATTTTGAAAA CAGCAATAGA AGTAAGATCC TTTAAGCTCT | 100 |
|    | ATTTCAGCC CCTAAGAAAA GTGATGAGGA CACTGTGCAT GCCCATATGT  | 150 |
| 30 | GAACATGGTG GTACCTTAGG NATTTCCCTT TNTCNATGAA TATA       | 194 |

## (2) INFORMATION FOR SEQ ID :247:

|    |                               |
|----|-------------------------------|
| 35 | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 249 base pairs    |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |
|    | (D) TOPOLOGY: linear          |
| 40 |                               |

138

## (xi) SEQUENCE DESCRIPTION: SEQ ID :247:

|    |   |     |
|----|---|-----|
|    | GGCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT | 50  |
| 5  | GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG  | 100 |
|    | CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT  | 150 |
|    | GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA  | 200 |
| 10 | GGCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCTT   | 249 |

## (2) INFORMATION FOR SEQ ID :248:

|    |                               |
|----|-------------------------------|
| 15 | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 248 base pairs    |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |
|    | (D) TOPOLOGY: linear          |

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :248:

|    |   |     |
|----|---|-----|
| 25 | GGCCCCCTCAA GGGCATCCTG GGCTACACTG AGCACCAGGT GGTCTCCTCT | 50  |
|    | GACTTCAACA GCGACACCCA CTCCTCCACC TGACGCTGGG GCTGGCATTG  | 100 |
|    | CCCTCAACGA CCACTTTGTC AAGCTCATTT CCTGGTATGA CAACGAATTT  | 150 |
| 30 | GCTACAGCAA CAGGGTGTGG ACCTCATGGC CCACATGGCC TCCAAGGTAA  | 200 |
|    | GGCCCTGGAC CACCAGCCCC AGCAAGGCAC AAGAGGAAGG AGAGACCC    | 248 |

## 35 (2) INFORMATION FOR SEQ ID :249:

|    |                               |
|----|-------------------------------|
|    | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 82 base pairs     |
|    | (B) TYPE: nucleic acid        |
| 40 | (C) STRANDEDNESS: double      |
|    | (D) TOPOLOGY: linear          |



## (xi) SEQUENCE DESCRIPTION: SEQ ID :249:

5 GGAGGGGACC GCAGCATCCA GCCCTCTAAG GCCGGGCAGC GGTGCGCTTG 50  
GGGCAGAGCG CAGCGCAAGC AGGCTCAGTG TA 82

## (2) INFORMATION FOR SEQ ID :250:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :250:

20 GGGGCCCTCA GGACATCCAC GTGAGCGTCT GCCCAGCTGC ACTGATATTG 50  
TNTTGCAAAT CCAGATTTGT TGNCACTACT GATGGGCGCG TGAAACCAGN 100  
GAGAGATGCA CAAGATTTAC AGGCC 125

## (2) INFORMATION FOR SEQ ID :251:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :251:

GGCCCAGAGG TCCTTTACTC TTACGGNACA CCTTAGCCAC ATTCACAGGG 50  
40 AATGNTCCAG CACTCAGGCT CCTTCCCATN GGTTTTCAAA AGCGCGTTTT 100  
TCTGGGGGAG CGGCCGCCTT TAGTCGACCC 130

140

## (2) INFORMATION FOR SEQ ID :252:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 216 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :252:

GAGAAGGCTG GAGAAAAACC ATCCACACAT AAACAATNGN ATTTACTCNA 50  
AAATNAAGTA CAGGTTTCAG GTATTTAAAA TAAATAAAGA AAAATCTCGT 100  
TTCCTTTGGC ATCTTTAGAA AATAAACTAA GCAATAAAAG AGGTGATTGT 150  
ATAAAGACAT GCGTAAGCAA ACATATGGGG AAAACCAGCA ACTTGGTTTT 200  
ATGNGATAAT ATCAGC 216

## (2) INFORMATION FOR SEQ ID :253:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :253:

GGAGAAGGAG GCTGATTGCG TACATCCAGC AGTTACAATT TTTAAAAATT 50  
ACANTNNNNC NNTTNGATTN TTAATNTANG TAATTCCTT CCAAAGAAGN 100  
TTCACATGTA ATAAGTAGAA ATTCTGTATA GGAAAAAAGC ATTAAAAATA 150  
TANATACNGC TTCATNCGTT GGGAACCATT AAAAGTAATA TAATNAGCTT 200

141

TTTTCAGAAG GATCTTTTGT AGCAGTGNTT ATGAATGNAC CCGCAAAAT 249

(2) INFORMATION FOR SEQ ID :254:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 166 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :254:

15 GACCCCATTC TATATTATNC GTNNNGCGAT TTTTtagcca CCCTGAAGTT 50  
ATATTNTAT ACCNAGGCTT CGAATAATCT CATCNGACTN ACCACCCTNG 100  
GAAAAAAGA ACCGTTTGAT ACATAGGNAT GNTNAGCTTG ATATCAATNG 150  
20 CTCCCTGGGN TTCTTG 166

(2) INFORMATION FOR SEQ ID :255:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :255:

35 CCAGACCAAC CGCCTGCAGG AGGCTCTGAA CCCTCTTCAA GAGCATCTGG 50  
AACAACAGAT GGCTGCGCAC CATCTCTGTG ATCCTGTTCC TCAACAAGCA 100  
AGATTTGCTC GCTGAGAAAG TCCTTGTTGG AAATCGAAGT TGAGGACTAC 150  
40 TTTCAGAATT TGCTCGCTAC ACTACTTTGA GGATGCTACT CCCGAGCCCC 200

142

CTTCTNTTGT NACAGACAGC AGA

223

## (2) INFORMATION FOR SEQ ID :256:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 292 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :256:

15 GGAGAAGAAG GAGCAGGAGG TGATGCTACT GACTCAAGTC AAACAGCTCT 50  
TGATAATAAA GCTTCATTGC TCCATTCAAT GCCTACTCAC TCCTCTCCGC 100  
TCTCGAGACT ATAATCCATA TAACTATTAA GATAGCATCA GTCCCTTCAA 150  
20 CAAGTCTGCC CTCAAGGAAG CCATGTTTGA TGATGATGCT GACCAGTTTC 200  
CTGACGATCT TTCCCTAGAT CATTCTGACC TGTGTAGAG TTGTTGAAGG 250  
25 AGCTGTCTGA CCATAATGAG CTGTAGAAGA AAGAAAAATT GC 292

## (2) INFORMATION FOR SEQ ID :257:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 238 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :257:

40 AAGGAGCAGG AGGTGATGCT ACTGACTCAA GTCAAACAGC TCTTGATAAT 50  
AAAGCTTCAT TGCTCCATTC AATGCCTACT CACTCCTCTC CGCTCTCGAG 100

143

ACTATAATCC ATATAACTAT TAAGATAGCA TCAGTCCCTT CAACAAGTCT 150  
GCCCTCAAGG AAGCCATGTT TGATGATGAT GCTGACCAGT TTCCTGACGA 200  
5 TCTTTCCTA GATCATTCTG ACCTGTTGTA GAGTTGTT 238

## (2) INFORMATION FOR SEQ ID :258:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :258:

GGAGAGAAAA GTTCCTGAGT GACAGAGAAA AAGAACAAAA AGCTGCAGAA 50  
20 GGCNTCAGCA GAGGCCACTG CTGGCCCTGA GGCTGCACCA AGTGACGAAG 100  
AACCGGCTCC AAGCATTCGT CACAGCACTA ATTTAAA 137

## 25 (2) INFORMATION FOR SEQ ID :259:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 241 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :259:

GCGCGACTTT TAAGGGATTT GCNGTGATGC CTGTTGACCC AGTGCCTTCC 50  
TAGCCGGGAA GGGGCTCGGC TGGAGTGNN AAGGCTCAGAA AAATTCGCG 100  
40 AAGAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT 150

144

TTTTGGACAG GTGGGTGCGG TGACCTTGGT ATGTATTTT CGTGTTACAT 200  
CGCGCCATCA TTGGATATGT TAGTGTGTNG GTTAGTAGGT C 241

5 (2) INFORMATION FOR SEQ ID :260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 248 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :260:

GCGGACTTTT AAGGGATTG CNGTGATGCC TGTGACCCA GTGCCTTCCT 50  
AGCCGGGGAA GGGGCTCGGC TGGAGTGNA AAGGCTCAGA AAAATTTGCG 100  
20 AAGAAAAAAA CCTATGAGGT AATAATAGGA TTATTCCGTA TCGAAGGCCT 150  
TTTTGGACAG GTGGGGCGGT GACCTTGTA TGTATTTTTC GTGTTACATC 200  
25 GCGCCATATT GGTATATGTT AGTGTGTTGG TTAGTAGGTC TCGTATGA 248

(2) INFORMATION FOR SEQ ID :261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :261:

GGATCTTTCA GGTGATGAAA TAGTTCTGTA TCTTGATTTT GGCGAATCTA 50  
40 CACANGTGAT GAAGTAACGT GATAAATGA CATAGACCTG TATGCCTACT 100

145

ACAATACAGT ATCAAAACCA GGGATTGATT CCTGGTTCTT TTCCAAATCC 150

ACTTCCCAAA CTTATGGTAA GGTAATATTA AAAAGGCACC AAAGAGCCCT 200

5 GATCCCTGGA TAAACAGGAT CATTTCAAAG NNGTTTATA 239

(2) INFORMATION FOR SEQ ID :262:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 143 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :262:

GCCGGGTGAT GGCCAGGAAG GTGCCCTCTG TTTTGTAA AACAGCCATT 50

20

GGCCTTTGTC ATTGAGTCAC CACCTGCAGG GCTTGGGAGT GAGCGTTGGG 100

TAGGNTCAGG CCCCCAGAAC CGCCTGGGTA CTCACCGCTA GCA 143

25

(2) INFORMATION FOR SEQ ID :263:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 246 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :263:

GGCGCTCAGC CTCCCCAAGG ACAAGCTCCT CCCCCTGTAA TACCTCCTCC 50

TAACAGCCGG ATATGGATGG CAAGTTACCA AACACAGTGA GCCGGGACTC 100

40

TAAAAAATA TAGCAATCCA GATAGGCTTC GATTTCCTG GACACTCTGA 150

146

AGACATGAAA GTAGACATCG AAAATGAAAA TANTTATNNA AATGAAATGT 200

TTGGAACCTT TAGCACAGAT TTGTTTGGGA AGACACGGTC TTTTAG 246

5 (2) INFORMATION FOR SEQ ID :264:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :264:

GGCTCCATTA AGGACCAAAT TNATGCTACC ACTAAACAAA AANNTATAGT 50

CTGTGTTAAA TCGTATGCTT TTTAAAGGTA TTTAAAGATT CAACTAGCTT 100

20 TAAAGAGGCT GAGCAGCTCA GGAAGCCTGT AATGTGACAT AACTCTTTGG 150

ACCTGATCTT GATGTTCTGC TGTGTNAGT CTTGAAGAGC GTATNTGAT 199

25 (2) INFORMATION FOR SEQ ID :265:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 245 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :265:

GGTTTCAATC GTCCATCCAA GATACAAGAG AACGCATTGC CACTGATGCT 50

TGCTGAGCCC CCACAGAACT TAATCGCCCA ATCTCAGTCT GGTACTGGTA 100

40 AAACAGCTGC CTCGTGCTG GCCATGCTTA GCCAAGTAGA ACCTGCAAAC 150



147

AATATCCCGT GTCTTCTCTN TCCCAACGTA TGAGCTGCCC TCCAAACAGG 200

AAAAGTGATT GAACAAATGG CAAATNTTAC CCTGAACTGA AGCTG 245

5 (2) INFORMATION FOR SEQ ID :266:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :266:

AGGAAAAGAT GGGAAATATGT TTCTTTCCTT TGAGAATTCA CAAAANGGGG 50

TCAAAAACAA AGCAATGCTG AAAGCGAACA TCCATTNGC CTGCAATTCA 100

20 AGGCGAAAAT CCAAAGGCAT C 121

(2) INFORMATION FOR SEQ ID :267:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :267:

35 GGGTCGCTCT CCCCCCTCT TTCTTCGGGT TGTGTGCGTC TCCGCTTTCG 50

TGATGTGAGG AACTCTGGGG TGGGCGACGG GTCCAACTCG CGTTGTCATC 100

TCCCAGGTTG GTACACCCCC CCCCCGTTTC CCCAGCCACA CTCCACGGCC 150

40 AGGCTGGAGG CAGATGTCT 169

148

## (2) INFORMATION FOR SEQ ID :268:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :268:

TCGCAGGAGA GGAATTACAT GCTCATCCTA GAAGGGGGGG CTGACTGCAG 50  
15 GTGTTGCTGG GAAGCCTCTC CAGGCCTGGA GCTGGAGTAC CCGTCCTCAG 100  
CACTGCCAGC AGAAAAAGTT GTGATTCAAG GAAAGCACAT TGAATGCATT 150  
ATAGCAATCC CAGACCTAAG TTCGAAGTTG CTTTGTAACA AGTGCTGCCT 200

20

## (2) INFORMATION FOR SEQ ID :269:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :269:

AGGGGGGCGC AAGAGAGAAG AACTTCACAC TTCTTTATTG CTCAGCCTAG 50  
35 ATAGCAGCAG CTGGGAATAC GTAGGACAAA CAGGACGTCG AACAAATTAC 100  
TCCACTATAT TAATATTCAC TACACCACTT ATTCTTTCTT GAATTGTAAA 150  
CACTAAGTGT AGT 163

40

## (2) INFORMATION FOR SEQ ID :270:

149

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :270:

10

TCACACTTCT TATTGCTCAG CCTAGATAGC AGCAGCTGGG GAATACGTAG 50  
GACAAACAGG ACGTCGAACA AATTACTCCA CTATATTAAA TTCACTCACA 100  
CCACTTATTC TTTCT 115

## (2) INFORMATION FOR SEQ ID :271:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :271:

CCCGAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA 50  
GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNNGN 100  
NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC 150  
TGCAGAAATN CCTATGTGAC TCTTATAA 178

## (2) INFORMATION FOR SEQ ID :272:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

150

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :272:

CCCAGACCT GCGANAATGG TGCTGTGACG ACGAATAGCC ACGCATTATA 50

GGGTNTTNTG TTATGGGGGA CACTCTACTA CGGGATGCGT ATGATGNNGN 100

10 NCCATTATNG NAGTGGGCAT TGGGGGGAAA CAGAGCACCT GATGCTTTAC 150

TGCAGAAATN CCTATGTGAC TCTTATAA 178

15 (2) INFORMATION FOR SEQ ID :273:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :273:

CTCTAGTAAA AATGTTTGAG GAAACAAAAA TGGGGAAGAA GATCAGAACA 50

AAAANATTGT TAACACTGAC CGTCCTCATG CAGGTAGGCT ACTACCAACG 100

30 CTGGTTGTTA CTCCAGGAAA ATCGAGGTGA ACATC 135

(2) INFORMATION FOR SEQ ID :274:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 231 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

40 (D) TOPOLOGY: linear

151

## (xi) SEQUENCE DESCRIPTION: SEQ ID :274:

50  
TGTCGAGGAG AAGAAACCAC TTGATAACAC CCCGCGACAT CGTGGGGCTG  
5 CTTGTCACAN GAAAGCACCA TGTCGCAAT GGATTGCTGC AGGTGCTGCC 100  
GTTGCCTCCT CAGGGTCTGC TGAAAGTCAT CTTCTAGGGT CTGAACGACA 150  
TAACGCAGGA AAAGGACTCG CCCAGGCAGA GTTTGTCCCT CTCCTTCAT 200  
10 GACATAGGTG AGCAGTTTCC AGTCCCACTC C 231

## (2) INFORMATION FOR SEQ ID :275:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :275:

25 TCGCAGGAGA AGAAACCTNG TTGCTCCACA ATGCAACCAC ACTGATTTTC 50  
TCTTTTCTCT NNAGTTNTCC TTGTCTGTAA CAGGAATGTC CCTTACTATA 100  
GCAGGCGGAC ACGGCCATGG GTCAAGCACC CTGCTTCTGG AACTTGNNNG 150  
30 NCGTNCCCAC CATTGATTGA 170

## (2) INFORMATION FOR SEQ ID :276:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 315 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

152

## (xi) SEQUENCE DESCRIPTION: SEQ ID :276:

|    |  |     |
|----|--|-----|
|    | ATATGAAGGA GGAAATGGCT CTCACCTTCG TGAATACCAA GACCTGCTCA | 50  |
| 5  | ATGTTAAGAT GGCCCTTGAC ATGAGATTGC CACCTACAGG AAGCTGCTGG | 100 |
|    | AAGGCGAGGA GAGCAGGATT TCTCTGCCTC TTCCAACTT TTNTCTGAAC  | 150 |
|    | CTGAGGGAAA CTAATCTGGA TTCCTCCCT CTGGTTGATA CCCACTCAA   | 200 |
| 10 | AAGGACACTT CTGATTAAGA CGGTTGAAAC TAGAGATGGA CAGGTTATCA | 250 |
|    | ACGAACTTC TCAGCATTAC GATGACCTTG AATGAAAATN GTACACACTT  | 300 |
| 15 | AGCGTAGCAT ATTNA                                       | 315 |

## (2) INFORMATION FOR SEQ ID :277:

## (i) SEQUENCE CHARACTERISTICS:

|    |                            |
|----|----------------------------|
| 20 | (A) LENGTH: 209 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :277:

|    |  |     |
|----|--|-----|
|    | ACGTTCTGCG CCTTCCTAGG AGAGTCTTAC AGTGTGAGA TTTCACAAGC  | 50  |
| 30 | AATGCGAGTG TAAAATACCA GCTCTACAAG AAGCTAGGCT CTGTGACGGC | 100 |
|    | ATAGTTTCA GTAGCTTTAT CACAATGAAA CGAGAATTAT ATGACATGGT  | 150 |
| 35 | AGCAGAAATA GGCCCTTTCG TGNGCTGTTT TATTNCTCG GATNGTAGAT  | 200 |
|    | ATAGTAATC  | 209 |

## (2) INFORMATION FOR SEQ ID :278:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 base pairs

153

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :278:

10 AAGACATCCT AAGCTATGTT GAGGAGGGAG AAGATCTGAG ACTCAAGTTC 50  
TGCTGTAAAC CATGAGGTGA TTTAGTAGCT AAGTACGCCT TAGCCTTTTA 100  
GAGTCTT 107

15 (2) INFORMATION FOR SEQ ID :279:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 276 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :279:

ATGAAGAGAA AACCATCCTC CCATATGAAA ATATTTGCAG TAGGAGAACA 50  
CAGTGCAATA GGCTCCAAAA ATGGCTTTTA AGACCTTTGG NGGGGCAGTT 100  
30 ACTACTGCTT TAAAAGCCAG GTTAAAGTAT ACTCTAAGCA AAGATGACCG 150  
TAGAGCAGCT AGCTTCCTTT TCTATAANNA TAGGGAAAGC TCTCTCCATC 200  
35 GTCCATCAA TCAGCTCTAG AAGGTTTTTC TTTCCCNCT ATAAGTGCAC 250  
AAAGGGGAAA CACTGATTTT AAGCTT 276

(2) INFORMATION FOR SEQ ID :280:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 185 base pairs

154

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :280:

|  |     |
|--|-----|
| AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA | 50  |
| CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT | 100 |
| TAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATACA  | 150 |
| GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAAT                 | 185 |

## (2) INFORMATION FOR SEQ ID :281:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :281:

|  |     |
|--|-----|
| AGGAACAGGA TAGGTGTATG CATACTACGG CTAAGGAGAA ACAAGTCCTA | 50  |
| CATACCAGGG TAGTGAGAAC ATTACCGCAT AACAGGGAAC TGTGATTATT | 100 |
| TAAAAACGC AGAACTTATT TTATCCGTGC TTTAGAAATA ACTGTATACA  | 150 |
| GTGTTATAAG TTGAAAAGAA CTCAAAACAA CCAATA                | 186 |

## (2) INFORMATION FOR SEQ ID :282:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

40



155

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :282:

TGTGGGCTCA GTAATGTCCC CGCTGATGAC AATTTCGAGA GTCCATGTTT 50  
TATAGAAACC TTGAGGTCGG CCAGCCGTGT CTTGGCCAAT GAGATGTAGT 100  
10 TGTGAGGAGG GGGCGTACTT GGGGACCAGG GGTGGGTGGA GATGTGCCCT 150  
GTAGGCACAG GGAGACTCAA AAGCAGGAGT TNTGAAAGCG TAAATGGG 198

15 (2) INFORMATION FOR SEQ ID :283:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :283:

AGAAAAAGGT GAAGCGAAGC CCAAGGACAC CATGCTAAGG GCAAAAGTAA 50  
GAGACAGTCT CAGAACTGAG AGAATCGTGT CTTCTGCTTT TTGAAGTAGA 100  
30 CTGTCACACT CAGGCAGCCT GTCAATGCTG AATGTTAGGA CTTCTGTCTC 150  
CGCTGGAGAC ACGCCTGGGC AAGTCAGCGT TTAGTGTTTG ACAGCTTTCT 200  
35 CAGCTCCCTG ACTCCGTTTA CC 222

(2) INFORMATION FOR SEQ ID :284:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 162 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

156

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :284:

ATGGATCAAA CTACCTCTAT AATGAAGACT GTTCTCAAAA ACGCGAGGNA 50

ATGTGNGACG ACACTGACCT ATCAGACAAG AGGGCATGCC CCCCTGGCCA 100

10 CCTTTGNCGC TGTTTNTGCA ACGTTCGCAG TGNTACTCTG CGTGAACCGG 150

TAGACTGCTT GG 162

15 (2) INFORMATION FOR SEQ ID :285:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :285:

GGATCCANGC AAAGCCCCT CCTCCAGGGT GAAGTTTTTC TCCCGCGACA 50

GACAGCAGAC TCGAGCC 67

30

(2) INFORMATION FOR SEQ ID :286:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :286:

157

GGTCGGATCA GGTCAACCCGG CAGCAGCAGC TCTCGAGAGC TGAGGCACAA 50  
GGCAGGGGGCC CGGCTGTACA CCTGCAGGAC CCAGGAGAGC CTGTTGCAGT 100  
5 TCTTGTCGGA AGCGCCGAGA TAGCCACTCA GTGTCCCTGC AGCAGGAGCA 150  
GAA 153

## (2) INFORMATION FOR SEQ ID :287:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :287:

20

TACTACGGCT AAGGAGAAAC AATGTTCTTA CATATCACGG GTAGTGAGAA 50  
CATATCTGCA TAACAGGGAA CTGTGATATT TAAAAACAGC AGAACTTATT 100  
25 CCATCGTGCT TTAGAAATAA CTGTATACAG TGTATAAGT TGAAAAGAAC 150  
TCAAATAAC TGATATAAAT ACATCTATGT ATTAGAATTT AAAAAAGCTG 200  
CTTTCTGTGA AGTCAATCAG CTATATTAAA AATGACACAA ATCCAAAACC 250  
30 GATGCATGCC ATATANAAGG GACATTGNAA GTCCGCTCGC TGC 293

## (2) INFORMATION FOR SEQ ID :288:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

158

## (xi) SEQUENCE DESCRIPTION: SEQ ID :288:

AGGGTAAATG TACGTTGTTG AGTCACAGGC CTGCCAGACC TCTACTACCT 50  
5 CATTGTCCCC TCCGGTGACC AGTTCTGCCG TCACTGTCAG GAGAATGCCC 100  
GTGTTGAATC ACTG 114

## (2) INFORMATION FOR SEQ ID :289:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 290 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :289:

20

ATGAACCAGT GCCCGAGGTA CCCGGGTGTG GACCAGAGAA GTTTGCTGGA 50  
AAGGACGTTG CCAGGACTTA CACGTTTACA GATCCAGCAA CTGCTCTNCC 100  
25 CAGTGCCACA ACCATGGGGC GCCAACCACA AGCAGGAGTG CCACTGCCAC 150  
GCGGGCTGGG TCCCACCCNA CTGCGCGAAG CTGCTGACTG AGGNGCACGC 200  
AGCGTCCGGG AGCCTCCCTG TCCTTGTGTG GGGTATGGNG CTCTGGCGTT 250  
30 GNGCTGGTTA CCCTGTAGGA GTTANTGNCT ACCGGAAGCT 290

## (2) INFORMATION FOR SEQ ID :290:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

159

(xi) SEQUENCE DESCRIPTION: SEQ ID :290:

AACCGCTCTC CACACCGCTC CCACGAGCTC CAAGCTTAAA CGTCCAGATN 50  
5 NACTTTGTTG CTTTGCTGAT TTAAACAGCT TGATTCTAAG CNCTTACTAG 100  
TATCATNTGT GGCAGGACTT GNTCCATATC AGTGTTACTT TTGCTACTGT 150  
TTGTAGAAC GATGTACATG AATGAGCCT 179

10

(2) INFORMATION FOR SEQ ID :291:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :291:

TCTTTCATTT TGNCTGCCAA TCATTGTCAG AAATTTAGGG AAGTCAATTG 50  
25 TGCCATTACC ATCGGCATCT ACTATTAAT TATGTCCTGT AACTCTGCTT 100  
CTGTGGGATT CTGCCCAAGA GATCTCATT AAGTTCCCAA TTCTTTGTTG 150  
TTATAGTACC ATCACCATTT CGTTAAATAG TGAAAGAGCT TTTGAATC 199

30

(2) INFORMATION FOR SEQ ID :292:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :292:

160

GGAAGACCAT TCTGATCATC CTCACTGACG CCPGCGCAA GAGGGTGCTT 50  
TTCCTGAAGC AGCTGGCTGT GGCTTATACT CGTGACTGGA CCTCTGGNCT 100  
5 CAATTGAGTT CCTCAACGAA GACCACACCA GAAATTGTCA TTGCCACCTC 150  
AACCGAANNG ATATTACAAT GTAAAAA 177

## (2) INFORMATION FOR SEQ ID :293:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :293:

20

ATTGGTTTTTC CTCATCCACT GAGAATGCTG CTGGTTACTG CAAACGTTCA 50  
CCAACCANAG CTTTGGTCCA TACAGCTTTC TTCTAGATTN GGAGACTCTC 100  
25 AAGGACAGCA GGNGCTTTAA AATCCCTGGA CTGTGTTGAG AGGGCTTCTT 150  
TAGGCTTTTC ATGATGTGAA TAGCCAGTCA TGAACCTTGN GTCTGTTTCT 200  
TTTAGGCTCT TTTTGCAGCA GCAGAGCCAT GCTATNGAAG GAGTGAGAAC 250  
30 CTATGCGAGN GACCCNGTGN TTGNACTTGC CAGGGAGCTT GCGCT 295

## (2) INFORMATION FOR SEQ ID :294:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 78 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

161

## (xi) SEQUENCE DESCRIPTION: SEQ ID :294:

AATGATCCTT TTTTCGCTCT TACCTATAGT ACAAGTCCAT GATACTACTG 50  
5 CATATTTTAC CATTTTGNA AACTGTGAG 78

## (2) INFORMATION FOR SEQ ID :295:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :295:

ATTCTGTACC TGTTCTGAAC CTCGCCATAA GGGACTTGCA GCTTCGATTT 50  
20 GCTAACCTGA AATTCTGCTG CTGCCATGGA ACAAGCCTGG GCTAGCTTGG 100  
GGGAGGAGGA GAGACCATGT GGAGTAGAGC CAAGCTCTGG ACATTTGAGA 150  
25 GAGCCCGGTA ATA 163

## (2) INFORMATION FOR SEQ ID :296:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :296:

AGCTTAGAGC GGAACGGGTT CCACGTGCGG TACTCCTGCT TCACGCCGCC 50  
40 CTCGGTCACC GTGACGCGCC TCTCGCCGTA CACAGACTGG CCCGGCACCA 100

162

TGTTAGCGTG ACCAGCGCGT CCTCCGCCCC GCGTNAGATG AAGAGGCCCT 150

CGTGCCGGTG CGCTCCACCG ACACCACCAT GGCCCCCTC 189

5 (2) INFORMATION FOR SEQ ID :297:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 199 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :297:

GGAAACCAGC CCCTCACATC CTCCCTGAAC TTCCTGTCCC CACTCACACA 50

AGTGGTCCGG TGTCACCCTG CAGTTGGGTA TAGTCATAGG TACCATTGAT 100

20 GACGCCTTCT ACCTCGGCCA TGTAGGCCTT CCAGTCAACC TCTGTGTCTG 150

GAAGAAGACA AGATGATCTG GTTACTTTTG AGTCTAGAAC TTGTCTGCC 199

25 (2) INFORMATION FOR SEQ ID :298:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :298:

AAAAGATGAT AAATCCACCC TCNTGCTCTT AAAATCCCAT AAACGNTAGG 50

CTCTGGAGAA ACAAGTTGTT CTGTGAGGCC CTTGCCATCA ACACACTAAG 100

40 CAATCATAGT CCCCCAGAGC ACNAGATACT GCTAATGACC ATTANATNTT 150



163

GTATCATCAT GCTGCCTCCT GCATTGAAT T

181

## (2) INFORMATION FOR SEQ ID :299:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 314 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :299:

15 AACATTGTTT ATTCATCCAG CAGTGTGCT CAGCTCCTAC CTCTGTGCCA 50  
GGGCAGCATT TTCATATCCA AGATCAATTC CCTTTTTCAGC ACAGCCTGGG 100  
GAGGGGGTCA TTGTTCTCCT CGTCCATCAG GGATCTCAGA GGCTCAGAGA 150  
20 CTGCAAGCTG CTTGCCCAAG TCACACAGCT AGTGAAGACC AGAGCAGTTT 200  
CATCTGGTTG TGA CTCTAGC TCAGTGCTCT TCCACTACTT ATATNCGCCT 250  
TGGTGCCACC AAAAGTGCTC CCCAAAAGGA AGGAGAATGG GATTTTTTCC 300  
GAGGCATGTA CATT 314

## (2) INFORMATION FOR SEQ ID :300:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :300:

40

AAGAGTCCTG AAGGCATATC CAAGCCTGTT GTTCCTGCAG ACCTCATTAC 50

164

CACGCCAACA GAGAAGGCTG GACTGCTGCC CACATGCTGC TTCCAAAGGT 100  
TTTAAGAACT GCCTAGAAAT CTCGTGTAGG CACGAAGGGC TTGAGCCAGA 150  
5 AAGGAGAGAC AAGTGCAA 168

(2) INFORMATION FOR SEQ ID :301:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 142 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :301:

ACCCACATG CCCAGATGTC CACGNGCTTG CNATACGCCT CTTTGCAAAG 50  
20 GACCTCAGGG GACAGGTACC TGGTGTGCCA GCGAAACCAA ACCATGCCTG 100  
CTGGTTCCCC TGACCTCGAT AGCTAGGCCA AGTTTGCCAG CT 142

25 (2) INFORMATION FOR SEQ ID :302:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :302:

AGAATTCGTA ACTCATCCTA GAGTGGGCAC ATTTTAGACA TAGCAGGCGT 50  
GATGACCAAC AAAGACTGAA GTTCCCTATC TACGGAAAGG CATGACTGGG 100  
40 AGGCCACAA GGACTCTCAT TGAGTTCTTA CTTCGTTTCA GTCAAGACAA 150

165

TGCTTAGTTC AGATACTCAA AAATGTCTTC ACTCTGTCTT AAATTGG

197

## (2) INFORMATION FOR SEQ ID :303:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 236 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :303:

15 AGAATTGCAA CTCATCCTAA GTGGGCACAT TTAGACATAG CAGGCATGAT 50  
GACCAACAAA GATGAAGTTC CCTATCTACG AAAAGGCATG ACTGGGAGGC 100  
CCACAAGACT TTCATCGAGT TCTTACTTCT TTCAATCAAG ACAATGCTTA 150  
20 TTCAGATACT CAAAAACGTT TCACTCTGTC TTAAATGAAC AATTGAATTT 200  
AAAAGTTTTT GAATAAATGA TGAAAATTTT TTAAC 236

## 25 (2) INFORMATION FOR SEQ ID :304:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 220 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :304:

ATGTCATTCT CCTCATCCTC CGCATCTCCA CTGTCGTGCA CAAGGACCAC 50  
CATGTTTCCT TTAGTTCCCA GCACACGGGG CTCTGCAGTA GTGAATGAAG 100  
40 TCTAGCACAG CCACCGCCCC CATGCCAGG CTCAGGAGCA CACTGAGGTC 150

166

GTCCACCAAC ACACCGGGTA CGTCCACCGA GCCTCTCCAC TGCTCTGGCT 200

TTAGGCCTCC CGTACAAACT 220

5 (2) INFORMATION FOR SEQ ID :305:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 145 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :305:

AGAAGAAAGG ACAÇCATTAC CATCCATATT GACATCGCAT TTCCATAGAA 50

ATGCCAAAGA AAGAAGGTCC TGGGGTTTTT TATAGAAGCT CAAAAGNTC 100

20 AACCTTCGAT GCTATCCCCC AGCCAATAC AAAATCAGAA AAAGC 145

(2) INFORMATION FOR SEQ ID :306:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :306:

35 AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT 50

TNGCTTTTAC TGGCGTACAT ATGAGTGGAA TATAAACTGT ACACACNNNG 100

40 NGNTGATATA AACAGATNNA 120

(2) INFORMATION FOR SEQ ID :307:

167

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :307:

10

AGTCAAGGCA TTATGGTTTT TAATCTGAAA CTTAGAGAAC CCTTTAATAT 50

TNGCTTTTAC TGGCGTACAT ATGAGTGGA TATAAACTGT ACACACNNNG 100

15

NGNTGATATA AACAGATNNA 120

## (2) INFORMATION FOR SEQ ID :308:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 247 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :308:

ACTGCACCCA CCCCAAGGCC ATGGCAGGGT ATGGAGATGT CATTATCAT 50

30

AAGATGGACA GATAAGCTGG ACCAATAATT AAGATTCCAG CAGAGGGTGA 100

GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAATGA TGGCAACGTC 150

35

TTGCCTTCCT GGGGACAGGG AGCCCTATTC AAANANAGTC ACATCTGAGG 200

AGCCGGGGGT TATAACATCA AGTCTGTCCT TGACCTCACA AAGCCAG 247

## (2) INFORMATION FOR SEQ ID :309:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs

168

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :309:

AGGTAAGGTT GTCACGTGGA ACAACTGATA AAGGTCAGCT ATATATGTAG 50  
10 AGCTATATAT GTGAGTCACA AGGTGTGTGA CATACGTGTA TACGTATAAT 100  
ATGCGTT 107

15 (2) INFORMATION FOR SEQ ID :310:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 114 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :310:

GGAAGACCTC GCTGGACATC CTGCAGGGCC ACATGGTGGC TCTGCTTGTG 50  
ATTCTGGGGT CCACCCTCTC CAGTCAAGAG AACCCCCGTC GGGTTTAATG 100  
30 TATCAGGAAA GAGA 114

(2) INFORMATION FOR SEQ ID :311:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 237 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

169

## (xi) SEQUENCE DESCRIPTION: SEQ ID :311:

ATGGCAAATA GGAAGAAGCT CAGTATCCTC CTCCCACCAT AACCCCACTC 50  
 5 TCCACTGCCT CCTGGACCAT AGTTTCCTCC ACTATACGGT CCCCCCATGT 100  
 TCCTGCTACC ACCAAAGTTT CCACTCTTTA TCGAACCGTA TTAGAAGGTC 150  
 GCTGGTTATA ATTTCCAAAA TATGTAATTT CCACTTCCAA ATCCTTTATA 200  
 10 GTTGTCTATA CCACCTCCGT AGCCCCCACC CTGTTGC 237

## (2) INFORMATION FOR SEQ ID :312:

15 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 147 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :312:

25 TNNTCCACAA CAGNGGGACT ACTGAAGACT AGAGAACGCC TCTGTGNGAG 50  
 TGGTGCAGAC AAAGACCTCA CTAAAGTGNG CTTAACAGAG TACTAGAGGA 100  
 GAGAACTTGG CAATAGCAAG TACAGACAAC TATGTGAGAA ATACTGC 147

30

## (2) INFORMATION FOR SEQ ID :313:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 151 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :313:

170

.. CACAACAGNG GGACTACTGA AGACTAGAGA ACGCCTCTGT GNGAGTGGTG 50  
CAGACAAAGA CCTCACTAAA GTGNGCTTAA CAGAGTACTA GAGGAGAGAA 100  
5 CTTGGCAATA GCAAGTACAG ACAACTATGT GAGAAATACT GCTCCCAAAG 150  
G 151

## (2) INFORMATION FOR SEQ ID :314:

10

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 287 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :314:

20

GAAGGTTGTA CGTGGACACT ATAAAGGTCA GCAAATTGGC AAAGTAGTCC 50  
AGGTTTACAG GAAGAAATAT GTTATCTACA TCGAACGGGT GCAGCGGGAA 100  
25 AAGGCTAATG GCACAACTGT CCACGTAGGC ATTCACCCCA GCAAGGTGGT 150  
TATCACTAGG CTAAAACTGG ACAAAGACCG CAAAAAGATC CTCGAACGGA 200  
AAGCCAAATC TCGCCAAGTA GGAAAGGAAA AGGGCAAATA CAAGGAAGAA 250  
30 ACCATTGAGA AGATGAGGAA TAAGTAATTN ATATANA 287

## (2) INFORMATION FOR SEQ ID :315:

35

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear



171

## (xi) SEQUENCE DESCRIPTION: SEQ ID :315:

GGAATCAAAC GNCTCTATAA TGAAGATAAT GTTCAGAAAA CGTGGGTTCT 50  
5 GTGGTGACAC TGATTTATCA AGACAAGAGG GACATGCTTC CCCTTGTTCCA 100  
CCTTTGCAGC CTGTTTCTGT CATGTAGTTT CAACAAGTGC TACCTTGAGT 150  
GTAAACTAAG GTAGACTACT CTGNGAATAA GAA 183

10

## (2) INFORMATION FOR SEQ ID :316:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :316:

GGAATGAATC AAACGNCTCT ATAATGAAGA TAATGTTTCA AAAACGTGGG 50  
25 TTCTGTGCGT GCACTGATTT ATCAAGACAA GAGGGACATG CTTCCCCTTG 100  
CCACCTTTC AGCCTGTTTC TGTCATGTAG TTTCA 135

## (2) INFORMATION FOR SEQ ID :317:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :317:

40

CGTTTGAAAT TCATCCCAAC TGTAGGCTGA GTGACCTGAA GTTGACAGAC 50

172

TGCCGAAGTC CAAAAGCTTC AGCATTTCTT TAGTGTCAGG ATCTACTTCA 100  
ATAATNNTGA TCCAAGGCTG AGACCTCAGA AACATAATGC TCTCCTTTCC 150  
5 CTATNTTTTC TGCGGCTTGA TGGAGATACC TTTACTG 187

## (2) INFORMATION FOR SEQ ID :318:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :318:

20 TCCCAGGAGA AGGAACTTTG AAATTCATCC CAACGTAGGC TGAGTGACCT 50  
GAAGATTGAC AGACTGCCGA AGTCCAAAAG CTTCAGCATT TCCTTAGTGT 100  
CAGGATCTAC TTCAATAATN NTGATCCAAG GCTGAGACCT CAGAAACATA 150  
25 ATGCTCTCCT CCCTTNCTTT TCTGCGCTTG ATGGAGATAC CTTTCACTGT 200  
GCCTCTCTGA ATCGTTTCAT CAGATGCTGA CGTAACCTGC TATTGTTGN 250  
AGCTTTCNGT TGNNNTAA 268

30

## (2) INFORMATION FOR SEQ ID :319:

(i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :319:

173

ACTGCACCCA CCCCAAGGCC ATGCAGGGTA TGGAGATGTC ATTTATTATA 50  
AGATGAACAG ATAAGCTGGA CCAATAATTT ACAGATTCCA CAGAGGGTGA 100  
5 GGACACCCAG ATGCGCCAGG ACTGTAGGAA ATCACAAT 138

## (2) INFORMATION FOR SEQ ID :320:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :320:

AAATGATGAT AAATTCATCC TCTTCTGCTC TTAAAATTTC ATAAACCTCA 50  
20 GGCTCTGGAG AAACAAGTTG TTCTGTTGGG CCCTTGCCAT CAACACACTT 100  
GTAATCATAC TTCCCCCA 118

## 25 (2) INFORMATION FOR SEQ ID :321:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :321:

AGAACAGTTG AAGGTCTGAG GTGTTGAGAG GCAAATGGGG TCTCTGGGTG 50  
GATCCTGGTC CTGTCAGCAG GCCTGGACTT GTTCAGGATG GACTGGTGGC 100  
40 GTTATAAAGG GCAGATCAGG GTGCCTGTCC CTTGGCATGT CCCTTAAGAT 150

174

TTCCTTTTCC

160

## (2) INFORMATION FOR SEQ ID :322:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :322:

|    |  |     |
|----|--|-----|
| 15 | AGGAGGGAGT TAATCCAAAC CACACAATGA AGTCTTCAA CCACCNCCCG  | 50  |
|    | AACAGGGCTG CTGATTGTTT CTTTCACTTT TGNGGTGACC TTGAGCTCCC | 100 |
|    | TTAAAAAAA AACTTGGAGA ATCACAACG GCAATGCACC GCAGTTCTCG   | 150 |
| 20 | AACTACACAA GCATAGTCTG ACTAAGTCAC ATGTGTTTCC ATATCAACTT | 200 |
|    | GTTTGACAGG GCGACCTACT GCAAAGCAGG CTCAGTTACC CCACCAGTCA | 250 |
| 25 | ACCCCTGGG AGTATAATNN TCTCCATANA A                      | 281 |

## (2) INFORMATION FOR SEQ ID :323:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 99 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :323:

|    |  |    |
|----|--|----|
| 40 | GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC | 50 |
|    | ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTG  | 99 |

175

## (2) INFORMATION FOR SEQ ID :324:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :324:

GGAATTTTCT CAAAGAAAAC GCAATAGCCA ATTGGAACCT ACTNTANCGC 50  
ANTTTATNNN GTCTTCTTTA ANNTAGAGTG ACTTACTGAT TTATTATTGA 100  
CACNNGTCCN NNGCNCNAGN TTACCATCCT TATGTGAATA CTNCAAGGGA 150  
TTGCCCGCGT TTTTAGG 167

20

## (2) INFORMATION FOR SEQ ID :325:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :325:

TGATCCAACT CTCCTGTGT GAAAAGAAGA ATGATGGCAG GAAGAACATA 50  
AAGACTTTAA AACTCCTAGC CGGGGTTTGT CGGACTCTTT GNCAGTAGTG 100  
ATTTAGCCAA CCAGGCAACA GAGATACGAT CTAATCTCCT CGCCCCCTCTT 150  
TCGGGTCGCG 160

40

## (2) INFORMATION FOR SEQ ID :326:

176

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :326:

10

GGAAGGGGTG TTGTTTGATA GACATTATCT GTGGCTGGGT CTTTCTGGCT 50

GATGAGAGAC ATGTAGATTA TGTGAAGCAA GTGGCTAGAA GATGAGAGAG 100

15 AACATGAGAG AGCAGAGTGC TCTC 124

## (2) INFORMATION FOR SEQ ID :327:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 253 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :327:

AGCCTAGTTT GAACATCCTC ATCCNGTGT TAGACCGGAT CCGATATACA 50

30 GAGTCTTAAG GAAATCGCAT CAACGTGCCT GAGCAGTCGG CTGTGACTCT 100

CGACAATGTA ACTCTGCAAA TCGATGGAGT CCTTTACCTG CCATCATGGA 150

35 CCCTTACAAG GCAAGCTACG ACGCGAGGAC CCTGATATGC CGTCACCCAG 200

CTAGCTCAAA CAACCACGAG ATCAGAGCTC AGCAAACCTCT CTCTGGACAA 250

AGT 253

40

## (2) INFORMATION FOR SEQ ID :328:

177

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :328:

10 GAACCTCTGG GCTCTCATCC TCTCCTATTG ACAGTGAAGC CCATGGCAAA 50  
TAGAAGAAGC TCAGTATCGG CTCCTCCAC CATAACCGCG TTNAATCGC 100  
15 CTCCTGGACC ATAGTTTCCT CCACCATAAG TCCCCCATG CTCCTGCTAC 150  
CACCGAAGTT CCCACTCCTG NGCGAACCGT AGTTAGAAGA TCGCTGTTAT 200

## (2) INFORMATION FOR SEQ ID :329:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :329:

30 TGACCTGATC ATCCTGAAAA ACTTTATGGG GGAGAAAGGT CAGCAGCTTC 50  
TCTTTCTTTT NTCGAAAATN ATAAACTGC GTATTCTACT TTATATTTAA 100  
35 TGTAAGGAAG AAAATATACA AGCCCATATT TACATCGTAT TTCTATTAAG 150  
AGCAACAATA GTTCATATGT TCATGTTTGC TACTATCACA ATNCAACATA 200  
TGAACACAGA TCAGCTCTAT ACCATGAATA CTGCTGGAAG TGATGGTTTA 250  
40 GGATTACCAA CTCCTGCTG CCATGACCGA 280

178

## (2) INFORMATION FOR SEQ ID :330:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :330:

CCTGAAAAC TTTATGGGG AGAAAGGTCA GCAGCTTCTC TTTCTTTNT 50  
15 CGAAAATNAT AAAACTGCGT ATTCTACTTT ATATTTAATG TAAGGAAGAA 100  
AATATACAAG CCCATATTTA CATCGTATTT CTATTAAGAG CAACAATAGT 150  
TCATATGTTT ATGTTTGCTA CTATCACAAT NCAACATATG AACACAGATC 200  
20 AGCTCTATAC CATGAATACT GCTGGAAGTG ATGGTTTAGG ATTACCAACT 250  
CACTGCTGCC ATGACCGA 268

25

## (2) INFORMATION FOR SEQ ID :331:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :331:

TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT 50  
AGAGTTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTTGCATTN 100  
40 TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC 150



179

TACCATATGC CCTTAAAAAT

170

## (2) INFORMATION FOR SEQ ID :332:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :332:

15 TCGCAGGAGA AGGAACCTAT ACACCCTTTA TAGAGCTTTA AATCGACTGT 50  
AGAGTTTTGT GGTCTTCCAG TCCCAAATGT TTAATTTTCC ATTTGCATTN 100  
TGAAATCACA TAACTCATGT CTGAAAAGTC CACCTGACAA GCATACCTGC 150  
20 TACCATATGC CCTTAAAAAT NNGGNNNNNG NNNNGGNTGA ANGTTCTGT 200  
GTTCCAAAA TNTAAGATTT GTT 223

## 25 (2) INFORMATION FOR SEQ ID :333:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 132 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :333:

AGACAATTGG CGGCATCCTC GTAGGCTTCA CTAATCCCA CAAGTTCTTC 50  
TGTTTTCATT TCGTTATTT TTTGCAGCCA ATTCTCTCCA TGTTGGCAG 100  
40 TCACAAGGCT CATGTGCTTC ACCAAGGCAC TC 132

180

## (2) INFORMATION FOR SEQ ID :334:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :334:

AAGTTGTTCA TGGNAGGCAT TTATCCTNTC AATAATNCAA ACGAGGCTTC 50  
TGGAATAACC AGTGCCCCAT TCCATCAGAG TCTTTGCGCG ACTAAAGCCT 100  
CCATNTTTGC CAATTTCAAT TGTTTGGGAT TCTAGCACTC CTTACCNGCA 150  
GTAATGCCCT TGCTGCAGAC AACAAACCTT GGACTGNGAG ATGGACCAAT 200  
TCTCAATGGC AATCCAGGGA AAGAGTGATC CTTCT 235

## (2) INFORMATION FOR SEQ ID :335:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :335:

ATGCCCCGAC CATCCGCTAC CCGATCCCC TCATCAAGGT GAATGATACC 50  
ATTCAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTCA TCAAGTTCCA 100  
CACTGGTAAC CTGTGTATGG TGAAGGAGGT GCTAACCTAG GAAGAATTGG 150  
GNGATCACCA ACAGGAGAG 169

181

## (2) INFORMATION FOR SEQ ID :336:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 193 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :336:

ATGCCCCGAC CATCCGCTAC CCCGATCCCC TCATCAAGGT GAATGATACC 50  
15 ATTCAGATTG ATTTAGAGAC TGGCAAGATT ACTGATTTC TCAAGTTCGA 100  
CACTGGTAAC CTGTGTATGG TGA CTGAGGT GCTAACCTAG GAAGAATTGG 150  
GNGATCACCA ACAGGAGAGG CACNCTGNAN TCTTTTGGCN NNG 193

20

## (2) INFORMATION FOR SEQ ID :337:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 307 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :337:

CAAAAGTCAT CCACAAGTTC TTTGTCTAGG ACTTCTAGCT GCTCAGACCC 50  
35 TCAGGGTCTT TGGATTGTTA CCAAAGTCTG TCAAACAGAC CAGTAGTTTA 100  
ATACCTGTAC AGAAAAATGT TTCTATTATG CTTCTAGTAT CTAGAAATTG 150  
CTTGCTACAG CATGGAGGTG GTTCTGCCTT TCCCTGGCTC CTCACACTCT 200  
40 CATCTGCAGG ATTCCCAGCT TTGCTCAGTC TTCATGCCCA CCAGAGGCAA 250

182

AAAGGCAAAC TAAAACTGTC ATGCAGTGGT AGGTTTGAAA TNAGCTGCTG 300  
CATCATG 307

5 (2) INFORMATION FOR SEQ ID :338:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :338:

AAAAGTCATC CAÇAAGTTCT TTGTCTAGGA CTTCTAGCTG CTCAGACCCT 50  
CAGGGTCTTT GGATTGTTAC CAAAGTCTGT CAAACAGACC AGTACTTTAA 100  
20 TACCTGTACA GAAAAATGTT TCTATTATGC TTCTAGTATC TAGAAATTGC 150  
TTGCTACAGC ATGGAGGTGG TTCTGCCTTT CCCTGGCTCC TCACACTCTC 200  
25 ATCTGCAGGA TTCCCAGCTT TGCTCAGTCT TCATGCCCAC CAGAGGCAAA 250  
AAGGCAAAC TAAACTGTCA TGCAGTGGTA GTTTGAAAT NAGCTGCTGC 300  
ATCAT 305

30

(2) INFORMATION FOR SEQ ID :339:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :339:

183

AATATAAAGA GGAAATGGCT CNTCACCTTC ATAATACCAA GACCTGCTCA 50  
ATTTAAGATG GCCCTTGACA TTGAAATCGT ACCTACAGAA AGCTTGNAAG 100  
5 G 101

## (2) INFORMATION FOR SEQ ID :340:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 113 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :340:

GTCGCAGGAG AAAAAAGTCG TCACGTCATG CGAGTGC GCA GGGGGCGTGG 50  
20 AGAGTAGCAG TAGAGCAACA AAGTACATAT AGGACAGTGC AGCGAGGACA 100  
AGGACTTCCC GCA 113

## 25 (2) INFORMATION FOR SEQ ID :341:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 209 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :341:

ACACAAATAA CTACATNTAC GCAATATAAT NTTTAAAAAT CCAGCAAT 50  
ATAAAGAGC AGAGCTAGGA CTGAACAGAA CATTTTGGTG TATAACCGGC 100  
40 AGCTCAAAAT CGCCAGCTGA TTGGAGTAAA ACTGATTCTA AGCGTATTAA 150

184

ATACGATTGA TTGTTTCCAT CACTAAGGGT GCCTATGAGT TTCTGAACCA 200  
TTTCTAGGG 209

5 (2) INFORMATION FOR SEQ ID :342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :342:

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50  
TTTtagacag GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA 100  
20 GCTTTTAATC TTCATTTTNN NNTTTGTNA TGGTAGGCTG AGATGCTTTT 150  
AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT 200  
25 TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC 250  
TA 252

(2) INFORMATION FOR SEQ ID :343:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :343:

40

GATCAANCAA AGCACAGGGA AAAGAGGCAA AATGATCACA GAAATCCGTT 50

185

TTTTAGACAG GTGTGACTTA CACTAACGAA AAAGAAAAAC ACATGAATAA 100  
GCTTTTAATC TTCATTTTNN NNTTTTGTNA TGGTAGGCTG AGATGCTTTT 150  
5 AAATGTGATG TTATAAGCCT AAGGCAGCTT GACTGCAGCA ACAAGTTTTT 200  
TACCCTCCTT GGCAAAGCAG GTCTCCTTAT GTAGCCTTGC AGCACTTCTC 250  
TACAAAAC 258

10

(2) INFORMATION FOR SEQ ID :344:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :344:

GAAGGAACCA GTGACCAGTC ATCCCCAGAG ATAGATGAAG ACCGGATCCC 50  
25 CAACCCACAT TCAAGTCCAC TTTGCAATGT CTCCACGGCA ACGGAAGAAG 100  
ATGACAAGGA TCACACCCAC AATGAAAGAG CTCCAGATGA TGGTTGAACA 150  
TCACCTGGGG CAACAGCAGC AAGGAGAGGA ACCTGAGGGG CCGCTGAGAG 200  
30 CACAGGACCC AGGAGTCCGC CCACCTG 227

(2) INFORMATION FOR SEQ ID :345:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

186

(xi) SEQUENCE DESCRIPTION: SEQ ID :345:

AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG 50  
5 TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC 100  
CTGGCACACT ACTAAACTGT AAATGTTTTT AAATCTGAAT CTGTAGAATT 150  
CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCA 188

10

(2) INFORMATION FOR SEQ ID :346:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :346:

AAATAAAAAA TAAGGTCCAA GCCAATGCCT AACAGATAAT AAGAGCTCAG 50  
25 TAAATGTTGA TTGAATACTA ACAAAGTAGT GAAAGCAGAC GACACAGTAC 100  
CTGGCACACT ACTAAACTGT AAATGTTTTT AAATCTGAAT CTGTAGAATT 150  
CTGTAAGGTT TTATGTAATA TGANGTCATT AGCTATCATG NCTCTGGATT 200  
30 NNCTNNNAGG TTTTAAGATG GAGCATCTGN GNATGTCAGC CCGTCCTATC 250  
TAGAAGTGNA AA 262

35

(2) INFORMATION FOR SEQ ID :347:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



187

## (xi) SEQUENCE DESCRIPTION: SEQ ID :347:

5 CTCTGTTTT CAAACGCCCA TGTGTGCTAT ACTACAATC TTCTCGAGTC 50  
TGATCAATTT GCAGTAGACC ATTTAGTTC TTACGACGTT AATAACAAAC 100  
ACTTCAACAT CANTGCTCCA ATCTGAAGTT CTTGTTGCAT TGTAAAAGA 150  
10 AATNTCTAA 159

## (2) INFORMATION FOR SEQ ID :348:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 283 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :348:

25 TCGCAGGAGA AGGAAGCTGC ATGCACTGA AAGGCATGGC CTGTCTCCTC 50  
ACTGAGTGCA AGGTCCATCG ACCAAAGCCC TGTTCTGATC AATAACATCT 100  
ACAATCGCAC CAATTTTCCG GCATGAGGTC CAAAGGAGAC ATAGGCCACC 150  
30 CGGCCAACCT CCACGAAGCG CCTGAACACC ATGCGCTTCC CGGGACCCTC 200  
TGGGAGCCGT TCGCNCCTCA GCTTCCCAGC GAGGTGGAGG TCGAGCGGCA 250  
TGGNCGACGC CCCGGAGCCC ACAACAGTAA GAC 283

35

## (2) INFORMATION FOR SEQ ID :349:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :349:

5 CAGAAAGGAG GCATTGAGCA AAAACTAGGA AAATCTGAAT AAACNGTGGA 50  
CCTCGCTTGG TTAATATATT TANACTGGTG ACTCATTTTA AAACTTTCCC 100  
GGGCGCGATG GCTCATGTCT GCAATCCCAG CACTTGNGAG GCTGAGCGGG 150  
10 TGGATCACCC AGGTCAGGA 169

## (2) INFORMATION FOR SEQ ID :350:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :350:

25 GAAGNAACCA GTACCAGTCA TCCCCAGAGA TAGATGAAGA CCGGATCCCC 50  
AACCACANT TAAGTCCACT TTGCAATGTC TCCACGGCAA CGAAGAAGAT 100  
GACAAGGATC ACACCCACAA TGAAAGAGCT CCAGATGATG GNGAACATCA 150  
30 CTTGGCAACA NCACAGGAAG GGACC 175

## (2) INFORMATION FOR SEQ ID :351:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

189

## (xi) SEQUENCE DESCRIPTION: SEQ ID :351:

AAATAAAAA TAAGNACCCA ACCAATGCTA CAGATAATAA GAGCTCAGTA 50  
5 AATGTTGATT GAATCACTAA CAAAGATAAA AGCAGACGAC ACAGTACCTG 100  
GCACACTACT AACTGTAAAT GTTTTAAAT TGAATCTGTA AAATTGTAA 150  
GGTTTTATGA ATATAATATT ATTAATATT ATGTCTCTGA ATTTTNNNN 200  
10 NAGGCT 206

## (2) INFORMATION FOR SEQ ID :352:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 76 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :352:

25 AGACATACTG TAGTGTCTAA ATAATATTTG TCNGAAGATA ACAATTATGG 50  
GACTTTAAAG CCGACAGTGA AATTAT 76

## (2) INFORMATION FOR SEQ ID :353:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 245 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :353:

40 ACATTTGGCC CTCAGACTGT AATTTCATA CTACTNTGAC TGATACTAGA 50

190

100 TGACCTGGCT GCCTAGGGGC TGTGCTGGTC TGATTTTTTG TGAGACAAAA  
150 ACCACTCTAA ACCTCCTGGT GCACTGAGGC TGTACACACC GNCAGAACAG  
5 GGCCTGCGT TAAAAGTTT CTGACCAAGT GGTGACAACA GAGGNCAAAC 200  
245 GTAAGGCTGT CTGGATAAGT TGAACCTNGC TGANCGGTAG CACCA

(2) INFORMATION FOR SEQ ID :354:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :354:

20

50 GGAATCTGTG CCACACAGCT GCACACGACT ACTGGCCAAA GGACAGCCTC  
100 AGAACATCAT GAGCTGGCGT GACCTCATGA TGNNCCTCAN TGCTGTGGGG  
25 CTTCTGCTNG AGGCCAGCAG AGGCTCGTAT GACTACCTGT NAGACCTGCT 150  
179 CTTTGGGTTG AGACTTTTCA GNGACAACT

(2) INFORMATION FOR SEQ ID :355:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :355:

40

50 AAGGAACGNA TGACTTTCCA TCCCTTGAAC CAAGGCATGT TAGCACTTGC

191

TCCAGCATGT TGTACCATTT TCAACAGAAA TCGCACAAAT GCTACTGTGC 100

AAGGTGCAGC CAATTTTNTT GTAAGTGTGA TTTCTTACG 139

5 (2) INFORMATION FOR SEQ ID :356:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :356:

TCCAGGAGAA GGAAACTTC CACTTATAAC TGTNTCAGCC TGAATAAT 50

GAAGAGACTA GCAACACCTC CTGAACACAA GCCTANTGAG CCCAGTCTTT 100

20

(2) INFORMATION FOR SEQ ID :357:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :357:

AGAAGGAAAC ACCAAAGAAA CATCCAAGCA ATAAAGTGGG AGACTAACCA 50

35 AGATTTGGAC ATTGGAATGT TTACTGTTAT TCTTTAAGAA ACAACTACAA 100

AAAGAAAATG TCAACAAATT TTTCCTAGCT AACTGAG 137

(2) INFORMATION FOR SEQ ID :358:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

192

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :358:

|    |   |     |
|----|---|-----|
|    | AAGGAACAAG TGGGTCATTC TCACTAAGGC TGCCTGTCAC TGCAGTCTTG  | 50  |
| 10 | ATCAGCTTGT CAATTGATA CTTCAGCTTT TGGTCCAAGG GACGAAGCTT   | 100 |
|    | TTCCAAAACC GTTCGAATCT CTACCACTCT CAAAACCTGCA TCATGTCCCT | 150 |
| 15 | GAAGAGATCC TCCTGAGGCT TTGTCCAGAA TGAGGTGGGT CAAATNNANG  | 200 |
|    | GGNACATGAG CAGCAGCTGN TCTTTAAC                          | 228 |

(2) INFORMATION FOR SEQ ID :359:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 248 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :359:

30

|    |  |     |
|----|--|-----|
|    | CAGGAGCAAG GAGGCCATTT TGCTGAGCTC TCACAGCTGC TAGAGATGCT | 50  |
|    | CAATGACTCC CAATACAACC CAAAGAGACA AACGCTTGTT TTTTCTGCCA | 100 |
| 35 | CACTCACCTT GGTGCATCAG CTCCTGCTCG AATCCTTCAT AAGAAGCACA | 150 |
|    | CCAAGAAAAT GAATAAACA GCCAACTCG ACCTTCTTAT GCAGAAAATT   | 200 |
|    | GGCATGAGGG GCAAGCCCAA GGTCATTGAC CTCACAAGGA ATGAGGCC   | 248 |

40

(2) INFORMATION FOR SEQ ID :360:

193

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :360:

10

AGGCACCTGT GGAGCCATCC TCCTTGT TTTT AATCGTCCTG CTGCTGCTGC 50  
CGTTCCGTGT CGCGTCGCCC ACATGACCCT GAGGTCGCAA TGATGAGTCC 100  
TCTCTGGTCA GACACCGCTG GAAATGAATA CCAGGCCTGA CCTCAAGCAA 150  
CCATGA ACTA GCTATTAAGA AATACANNGG NAGGGCGGCA GCCGGATCGT 200  
GNNGGCGTTT NTCTGNGCCG CCCGTCTCAA TCTNTGTTCT GCTTCCAGAT 250  
GCC 253

20

## (2) INFORMATION FOR SEQ ID :361:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :361:

35

GAGAACCACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG 50  
GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTTT 100  
CTAAACNNGC TNGGCNATGT CGTAGTTNGT TGTCAGTNGA TCGGTAGAGA 150  
TAAT 154

40

194

## (2) INFORMATION FOR SEQ ID :362:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :362:

GAGAACCACG GGCTCCATCC TGGCCTCCTG TNCACCTTCG AACAGATGCG 50  
15 GATTAGCAAG CAGGAGCACA CGAATCAAGC CCCTCCAGCC ACCAAATTTT 100  
CTAAACNGGC TNGGCNATGT CGTAGTTNGT TGTCAGTNGA TCGGTAGAGA 150  
TAATCCTGNC CACGCCCT 168

20

## (2) INFORMATION FOR SEQ ID :363:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :363:

AAGGGATAAA AGGAAGCTTT GNCACCACTC TACCATCAAA NNGGAATTGA 50  
35 ACATTCCCAT TAAGGCAGTA AAACAAAAGC CAATAGCAAA CATGNATTTC 100  
ATTCAACCAT TGATAGATCT CTGCCGTTAT TCTTCAGTTT CTCTTCTCGT 150  
CTCTCTATTT NTTTCTCTGG TTGTGACCA GCTGACTNTG NCATCGTT 198

40

## (2) INFORMATION FOR SEQ ID :364:



195

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :364:

10

TTATACAAGT CAAACTTGGA AGGTCATAGT AAGCATACCT ATGCTGAGAG 50

AAAAGCATCA AATCCTCCGC GACACATCTA GTTCATCGTA ACAAAGCAAC 100

TCGTACACTT TCAAGTTTAA A 121

## (2) INFORMATION FOR SEQ ID :365:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 211 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :365:

GGTAAGTTGT ATTTGGGCCA GAATTTTAAA GAGCACTATT TCGACATTAA 50

30

AATGTATTCT TCTCGTATTA ATGCCTACAT CTCAGAGTT TTCAATGCTT 100

TCTAAAAGTT TCCTCTTGG AAAGAAGAAA TCTGAAAGAC CTATCATGCC 150

GTTCTTCCTG GCGTCTATAT TTCCTTTAGA GAGGCAAGGT AGGATTCCGT 200

35

CTCCAAGGGA G 211

## (2) INFORMATION FOR SEQ ID :366:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 base pairs

196

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :366:

CGGCTACAGC ATCACATCCA CTAAATGCAC AGTTGTTGAA GTCACGCCCT 50  
10 GCCAGACCTC TACTACCACA TTGTTCCCTC CGGTGACCAG TTTGTCCGTC 100  
ACTGTCAGGA GAATGNCCCG TGTCGAATCA TCGATCTCCA TCCGAGCCAA 150  
15 AAGTTTTCCA TATGCTGAAA TTACTGAATT GCCCTCGTTT ATAGTATATG 200  
ATACAGTGGC CTCGTTGGA GGCAGATATC AAGCATGGGG ATAAGCAGTT 250  
TTCTGGTCCT TAAGGGCTCT CAGCAAATCT CCGTG 285

20

(2) INFORMATION FOR SEQ ID :367:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :367:

GACACTGAGG CAGCTACTGA GAAGGGCAGA ACATGTCTCA ATCCATAGAG 50  
35 GTCTTGGCAG GCGAACCCAG AGAGACTTGC AGTACGTGAG AAGATGGAGA 100  
ACCAAATAAA AGGACTGGAG TCCAGTTCAA ACAAGGAGGG AGTGGTAGT 149

40

(2) INFORMATION FOR SEQ ID :368:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 137 base pairs

197

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :368:

GGTTCCCGCT CTCACAGCCA TTGCAGTACA TGAGCTCCAT AGAGACAGCG 50  
10 CCGGGGCAAG TGAGAGCCGG ACGAGCACTG GCGACTTGTG CCTCGCTGAG 100  
GCAATACTAT AATANGCAAG GAACTTTTGA GGCCGAG 137

15 (2) INFORMATION FOR SEQ ID :369:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 192 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :369:

GCCATCATAA GTTCAAAAGA AAAGAGAAAG TGTTATTTTT CTGTTAGTGA 50  
CATGTAGTCC CTTTGTCTA GTAGGAAAAA AGGTGCCTAG AGGTAGTATA 100  
30 TAGAGTAAAT ATTGTTCCCT TGCCTACTCG TGCTTCCAAT GATTAAGGAA 150  
ATGTAAACA NNNGTNAAAG TCTGTTTGT CAATGCGGGA GT 192

35 (2) INFORMATION FOR SEQ ID :370:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 197 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :370:

5 GAGACTTAAG TAAAACGGCT GCAGGCCAGA TCGCCCACC AGCTCAGAGA 50  
CCACCTTTAT CCATGCTTTG AAGTAGGACT CCTCCGTCT TCAAAATNTT 100  
GAAGACCCTA ACANGCTTTT ATGATGGGGG TCATATCTAT GGTACGNAT 150  
10 ATAGTAGAAA CCAAAAGAAT GTAAGTATTT GTNNATGATT TAAAAAT 197

## (2) INFORMATION FOR SEQ ID :371:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 114 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :371:

GCATCTGNCA GCTGCTGCAG GCTGACAGCC TCCAGACCTG GACAGAATTC 50  
25 ATACACTCCC GGAGCTGAAA AAACCGAACA TAAGGGAGTG CACAAGAGCC 100  
GGGCTTTGGA GAGG 114

## 30 (2) INFORMATION FOR SEQ ID :372:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
35 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :372:

CTTTCTCTAC TCCATCCATT ATCTCCGGGA TTCCTCCACA TTCCCTTCAG 50

199

CTCCTAGTTG TTCCACCTTG GCTAACAATT TACCAATCTT TTTTCTATG 100

AACACGTTCT GCCTTTGCTG CTA CTTC 127

5 (2) INFORMATION FOR SEQ ID :373:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 257 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :373:

AAGCGCTCAA TTCGCATCCA CAATGCAACC ACGAACTGAT TTTCTCTTC 50

TTTTTCAGTT CTCCTTGGTC TGTAACAGGA ATGCCCTTA CTCAGTAGCA 100

20 GGCGGACACG GCCATGGGTC AAGACACCCT GCTTCATGGG GAAACCTTGT 150

TTGTCGTTCC CACCACTGAT TCGGACCACA TAACCTTATN NNATCCCGAG 200

25 CGTTAGCAGC AACTTTTGTG GCCATACGCT TCTCATAGAA AGTACGAAGT 250

TTGGCAT 257

(2) INFORMATION FOR SEQ ID :374:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :374:

40

GCATCATCAT TGACATCCCT ATCAATGTCT ACGCTGCTGG CAGAGGACTG 50

200

100 NCCATTTGGA GCTGAGATGT GTAAGCTGGT GCCTTTAATA CAGAAAGCCT  
150 CCGTGGAAT CACTGTCTGA GTCTGTGTC TAGTATTGAC AGATATAGCT  
5 180 TTGTTCTTGG AGTAGAATTA AGGAATTGCG

## (2) INFORMATION FOR SEQ ID :375:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 323 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :375:

20 GGACCATTCT GATCATCCTC ACTGGACGCC ACAGGGGCAA GAGGGTGGTT 50  
TTCCTGAAGC AGCTGGCTAG TGGCTTATTA CTGTGACTGG ACCTCTGGNC 100  
TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT CATTGCCACT 150  
25 TCAACCAAAA TNGATATCAG CAATGTAAAA ATCCCAAAC ATCTTACTGA 200  
TGCTTACTTC AAGAAGAAGA AGCTGCGGAA GCCCAGACAC CAGGAAGGTG 250  
AGATCTTCGA CACAGAAAAA GAGAAATATG AGATTACGGA GCAGCCAAGA 300  
30 TTGATCAGAA AGCTGTGGAC TTA 323

## (2) INFORMATION FOR SEQ ID :376:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

201

## (xi) SEQUENCE DESCRIPTION: SEQ ID :376:

GGGGAATCCC ACCTCACCCA TTNGGTGAA ATGCTTTTTT CTAAGAGGTG 50  
5 AAATCACTCG CTGGTGTTHA TTTCGGCACA ACCAGAAAAT AGTGNGGGAT 100  
ATTGAATTAT GGGAGGCTCT GACTGTCTCG NGTGCAGCTT ACATTCACAG 150  
ATGGGGGGTA GTTTTATAT TCTATAAGCG AGCATATTAA ANGCAATATG 200  
10 AGTCAGTCCT GCATTTATGT CTT 223

## (2) INFORMATION FOR SEQ ID :377:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 122 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :377:

25 GGCTCAGGAT CCGGCATCCT TTATGCCTCC ACAGCACCTT GCTCTTTCCC 50  
CAGCCAATCA CTTTAGATGC TGAATCGATT TAAACANAT GTTTGTGCAT 100  
ATGGCTAATC AAGAGCCAGG TA 122

30

## (2) INFORMATION FOR SEQ ID :378:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 195 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :378:

202

GGCAGTGCCT GCTTCATCCC TTTATGAAGA ACAGAAAATT ATGACTACTC 50  
TACAAGGTGG ATAATACTTC GGTACCTTGC TTGCCACAGC CCTGTTTCCTC 100  
5 AAAGCTGAAT TGATAAATTT CTCTTTGACT TCCAAGACCT AGCAGTTATA 150  
AGGCGCCTTG AATAAAGTTT GTGCCTGAAA ATGTGGAGCA ATGCT 195

(2) INFORMATION FOR SEQ ID :379:  
10

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :379:  
20

GTAGCCCTGA GGTCACTCCTG CAAAGNGCGT ATCAAAAAAN ACGAAGTTAG 50  
GGTGACAAAG TTTGACAGTG ATGTTTACAA GTCAAACCTG GAAGGTTATA 100  
25 GTAAGCATAC CTANGCTGAG AGAAAAGCAT CAAANCTNNG GNACATANTN 150  
GTTTNTNGN AACAAAGCAA CTTGTAATTT AAGNTTAAAC NGAGCATCAT 200  
ATANNNNNGG 210

30  
(2) INFORMATION FOR SEQ ID :380:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 238 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40  
(xi) SEQUENCE DESCRIPTION: SEQ ID :380:



203

CTGGCTCACC TGGACAACCT CAAGGGCACC TTTGCCACAC TGAGTGAGCT 50  
GCACTGTGAC AAGCTGCACG TGGATCCTGA GAACTTCAGG CTCCTGGGCA 100  
5 ACGTGCTGGT CTGTGTGCTG GCCCATCACT TTGGCAAAGA ATTCACCCCA 150  
CCGTGCAGGC TGCCTATCAG AAAGTGGTGG CTGGTGTGGC TAATGCCCTG 200  
GCCCACAAGT ATCACTAAGC TCGCTTTCTT GCTGTTCA 238

10

(2) INFORMATION FOR SEQ ID :381:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 275 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :381:

GTCCTATGGC ATGAATGTTT GCAACCAACC CAGGAAAAGC CTTAAAGGAA 50  
25 ATAGCTGTTC ACATAGGAGA CCGTGACAAAT GCTGTACGCA ATGCTGCACT 100  
CAACACCAAG CAACGATGCA CAATGTACAT GAGGATCAGG TGTTCAAAC 150  
GATTGGAAAT CTTTTTGAAA AGGATATGAG CATGCTCGAG GAGAGGATTA 200  
30 AGCGTCAGCA AAGAGACCCT CTCTGCACCA ATAAAACAGG TGGAAGAAAA 250  
CCTAGCNCGC ACAGAACATA AGCTC 275

35

(2) INFORMATION FOR SEQ ID :382:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 96 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :382:

5 AAGCAGAGTA CGCACGTCAG GCCCTTCCAC GCCCAGCCCA ACACTTTAAA 50  
CNTACTGGGC GATGGGGCCG TTTNGCTGGC AGTTCAAGAT AAAACA 96

## (2) INFORMATION FOR SEQ ID :383:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 196 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :383:

20 GGACTTGATG GCTTCTTTCA AAGTCATAGA CTTGTGGTAA ACTTCTTGCA 50  
AGGAGCTCTG GGCACCCTCT GAAGCAGAGC CAATTGCTCG AGCATCACAC 100  
TGTACAAAGG TCCAGATGGG TTCATATGAA ACAGCTGGAG TCCTTTTCAT 150  
25 CAATNCNAAT NGANNGGTTA CTCCAAAGGG ACGAGACATG CACCTG 196

## (2) INFORMATION FOR SEQ ID :384:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :384:

40 AAGGAGGCCT TTGAGTCCCA TCCTCTGCCA CGCAGAGAGG CAGGCCTGGC 50  
ATTTCAGCCT CACTTTGTGT AGGTCACTTT TCGGTCTGTG TTGTAGCTCA 100

205

CCAACCAACA GTCAAACCCC AGCGTGGTAG CACGAGGTCC AGAACCTCTG 150  
CTTAGTGGGC CCGTATAATA AACGCAACCT GACCCAATTN NGGTTTCTTT 200  
5 CCCCAT 206

## (2) INFORMATION FOR SEQ ID :385:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 134 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :385:

GAATGCTTGG GATCATCCAG GTGNCTCTAT TTATAGGCAC CTGTGTTTAC 50  
20 CAGCAGTCTC TCTATTAGAA TGCTTGGTGT GCCAATGTTT CTTGAATTAG 100  
AAGCCTGGGG NCACCTAGGT GTTTCTATTA TAAA 134

## 25 (2) INFORMATION FOR SEQ ID :386:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 161 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :386:

CAAGGCCTTC CTGCACTGGT ACACGCCGAG GGCATGGACG AGAGGAGTTC 50  
ACCGAGGCCG AGAGCAACAT GAACGACCTG GTGTCCGAGT ACCAGCAGTA 100  
40 CCAGGACGCC ACGCCGACGA ACAAGGGGAG TTCNGAGGAG GAGGAGGCCA 150

206

GGACGAGGCG T

161

## (2) INFORMATION FOR SEQ ID :387:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :387:

15 GGTGAGCCTC CGCCATCCAG CCAAAC TGTGC TGAC CGCAGCTGTG 50  
CCGTGGCACG ATGGCGAGGA AGCCAGCCCC AAGGACAC TGAAAACACA 100  
ACCACTCAAT GCCGTGTGGT TTTGTTTGAA TATAAATNGC TGAAAGTGT 150  
20 GTTTTTTNAG GCAGTAATNT 170

## (2) INFORMATION FOR SEQ ID :388:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :388:

35 TCCATCTGAC ATCGCATTTT CATAGAAATG GCCAAAGAAA GAAGTCCTG 50  
GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTTGATG CTATCCCCCA 100  
GCCCAATACA AAATACACAG AAAAAGCAAT TATTAAAAAC GGCTTCGGTT 150  
40 TCTTTTTTCT CTTTAAATNNC CTACAATNGC TTTACATATT CGTGTGCAGC 200

207

ACCTACTTCT TTATGCCGTG AACTGAAATC TAAGATTTC AACTGAAATC 250

(2) INFORMATION FOR SEQ ID :389:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :389:

15 GCCATCTCCC CGCCACCCNC TCGTCCCCTT CTTNTCNGC CACCCTTCCT 50  
CNCTCNTCCG TTTTNGCTCC ACTCCACTCC TCCNTTTTNA GTACCCTCCT 100  
CNTTTATNTA GAGTTACTGA GAGCCGACCT GACGTCTCCA ACATNCCGTN 150  
20 TCTTATATCT CATCNCGGTT NTNGANGAAT GNAGTNAGGG TTCCGGGAG 200  
AGACCNAACT TGCTCTAGCC CTTTCCAGCC GCTGTTGTTA AACTGACCTC 250  
25 GTAGGGCNTG AGGGAGGT 268

(2) INFORMATION FOR SEQ ID :390:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :390:

40 GTCAGAGGCA GCCCATCCAG CACGTGCTAG GTGTTCCCAT ACGCACAGGA 50  
GAGGCGAGCT AGCCAGCCAA GGCGGGCAGG CGGGGAGGCC CTCTAGCTGT 100

208

TTGCCTCACC TGTGGGGCCC CAGCAGGGAG GAGTCACCAG CCTAGAGGGG 150  
CCAGGTATAC ACCTTANAGA GGATGAC 177

5 (2) INFORMATION FOR SEQ ID :391:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :391:

GCTCCACTTC CCACATAANA CNAGACCTCT CACAAAAGAG TTCACTGATA 50  
TGTGAATGCA GCTTTCTCCC CATGGTAGCC AGGACAGGGT GCACATTAAG 100  
20 GCAACCCCAA AAACACCTCT TNCTGNCTGC CTCTGCAAA 139

(2) INFORMATION FOR SEQ ID :392:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 259 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :392:

35 GAGGAGCTGC CCTCAAGGTC GTGCGTCTGA AGCCTACAAG AAAGTTTGCC 50  
TATCTGGGGC GCCTGGCTCA CGAGGTTGGC TGGAAGTACC AGGCAGTGAC 100  
AGCCACCCTG GAGGAGAAGA GGAAAGAGAA AGCCAAGATC CACTACCGGA 150  
40 AGAAGAAGCA GCTCATGAGG CTACGGAAAC AGGCCGAGAA GAACGCGGAG 200

209

AAGAAAATTG ACAAATAATA GAGGTCCTCA AGCCCCACGGA CTCCTGGTCT 250

GAGCCCAAT 259

5 (2) INFORMATION FOR SEQ ID :393:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :393:

AAAGATCATC AGTTTGGAAG GTACTGGTCC AATTTATCTA GGAAGTATCT 50

CTTGGAGTTT CAGAAATGCT AGCTTGGACA ACTGAAAAGT CACATCACAG 100

20 CTGGCATTCT GGGGGCTACC AAAACACCCC TCNNGGAGTA GAAGCTGCTG 150

GAAGGCAGGC CTGAGCCATT CACCACGGAC AGGAAGAGC 189

25 (2) INFORMATION FOR SEQ ID :394:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :394:

AGAAGGGGAG GTCGAAGAAA TGTGGCTGAT CATAAGAAAG GAGCAAAGAA 50

AGCTAGAATT GAAGAANNNN GAAAGAAACA GAGGACAAAA AAACAGA 97

40

(2) INFORMATION FOR SEQ ID :395:

210

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :395:

10

AAGAGGGGCT AAGACCCAAG TCATCCTCCA CTTTCGTTTT GTTATATTTT 50  
GCTTAGAATT GCCTCTTCTT CTCCACTTCA GAACTGCCTC AAAATTGACC 100  
CCCTTGACTG ATTTATTGTC GTCAAAGCA TGTCCTCTA TCTTTNNNN 150  
TCAGACGATC CGCTGCCTTT CTACATCTGA GAATCTTGTC AAGCATGGAT 200  
AAACTTGNTT TTATGTTGCA TATTTNACG GCTTCAACTT GAGT 244

20

## (2) INFORMATION FOR SEQ ID :396:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :396:

TAATATCGCC ATGTAATGGT ATACATTGTA AGGCTTATGT CACTAAAGAT 50  
TTTTATTCTG ATCTTCCAT AATAAAGGTC ATATGATACT GTATAGACAA 100  
GCTTGCAGT GAAGTATAGT AGCAATAATT TTCGTACCTG ATCAAGTTTA 150  
TTGCAGCCTT TCTTTCCGT TTCTTTNTG AAGGG 185

40

## (2) INFORMATION FOR SEQ ID :397:



211

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :397:

10

GGACACATCC ACCCAGTGAA CTGGACTGTG GCCATGACCC AGGGTATCAG 50  
CTCCAAACTC TGCCAGGGCT GAGAGACACA TGAAGGAAGA TGATGGGAGG 100  
AAAAGCCCAG GAGAAGTCCA CCAGGGACCA GCCCAGCCTG TATACTTGCC 150  
ACTTACCACC AGGACTCCTT GNTCTGCTCT GGCAAGAGAC TCTTGTCTGA 200  
ACACTGCTTA TCTGACCC 218

20

## (2) INFORMATION FOR SEQ ID :398:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :398:

GGAAGCAAAA AAACAAACT AAGCTCGAAT TTGCTTCAA ACCTGTAGAT 50  
TGCATCTAAC CANGTGTCCC TATGCACCTC AGAGTACTGG AATACGAACC 100  
CAGCGAGACC TTGTCCCCTC CCATTTTGCT GNACTTTTGT TGGTGAAAAT 150  
GAGAATGAGT TNATCCCTAC NTACTTAGTT TAATGCATTT GACCCCAGAA 200  
AACCCAGTA CCTTTNNACA ATGACCCAAC CANTACCTAC CATCGGCCAG 250

40

212

## (2) INFORMATION FOR SEQ ID :399:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 278 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :399:

TCAC TTGATT CATCCGTCGC GGGATTGGG AGCACTAGCA ACATAATCAA 50  
15 CACACTCCTA CAATCTTAGG CTTACATGT GCTGATGATG ATGAAACCAA 100  
CTCTGCCCCA ATCATCTCCC CTTCTNNTAG GGTCTTACTA CATATCGCAA 150  
CAGAAGATAA TATTGAGGTG AAGAGGGTAA CATGAAGTTT GGCAC TACCC 200  
20 TGAAGA AACTG TAGGCATCTC TTGGAATGTG CTAAGGAACT TGATGTCCAA 250  
ATAATGAGAT TAAATTTATG TTTCGAGT 278

## 25 (2) INFORMATION FOR SEQ ID :400:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 207 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :400:

GGCCAAACTC ACAGGAGCCT AGGCACAGAG CACTGAACAC TGGCTCTGCA 50  
GCGGGAAGGA ATTAGAGCCT TCTGCTTTTG CACCTGCTTT GAGTTAGGAA 100  
40 GCAAGCTCTC TTCCTTGCCA GACTTCCTT TGGGGCAGGA CACTTTTTTA 150

213

TACNCTGAGG CAAGGCAAAC AGTCATAGAA CAGTTATTAA ACAATANAAA 200

ATGTGTT 207

5 (2) INFORMATION FOR SEQ ID :401:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :401:

GAGGCATGGC CACATTCCAA GAAATGGAAT AAGGAGTGGG ACAGCAGGCA 50

GGGGGCCAGC CTGGGGCCTG GGCCTTTTAA TCTAAGGACT GGGGAGAACC 100

20 AAGGGACCTT AGAGGTCCTC CAGTCCTCCC CATATNNAAA GAGGGAGAAC 150

AAGCCTGGAG AGGAGGCTAC CTTAAGACCC TAAGAAGAAT TTAGCAATCG 200

25 NTTCTCCAAA GATAGCC 217

(2) INFORMATION FOR SEQ ID :402:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 225 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :402:

TTTACAATAG ATTTACCTT CANTTTAGTC AGAGTTGTTG ATTCAAGACT 50

40 CTTCCACAC TCGCACATCG AAACATTTTT GTGCCAGGGC TTTCCAGCTC 100

214

CAATTATCTT CTCGACAGCA TATACAGAAT CCCACATCT GGAACACTTC 150  
TCAGCACCTC CATANNTTGA GCAAATTTAG AAGTGTTTGG ATTTGTTGTA 200  
5 GGCCTGTGAG GCTGAACACT CTCTG 225

## (2) INFORMATION FOR SEQ ID :403:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :403:

AGAAGGGGCA TACTCGCTGG AGACCTGGTG CCTCTATCCA CTGNACGCTG 50  
20 ACTGNGGCTT CCACTGCGCC CGTGTACNTT ATCGAAGCTA CAGAT 95

## (2) INFORMATION FOR SEQ ID :404:

(i) SEQUENCE CHARACTERISTICS:  
25 (A) LENGTH: 239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :404:

AGGAAAAATT GACATTACTT GTTAGAAGAG CAACTCTGAA AGAAAACAAG 50  
CAAATTCCAA AACAGAAAAG ATTCACAATN NAAAGGTGCA TACATTAAAG 100  
GGCCCACTG TGTAATACTG TGCCAACTTA TGCAGTCTC ATTGTTTCAAG 150  
40 ATGAAATGTG AGATTGTAGT TTGAATGCTA TAAGCAGGTT CCAAGATACC 200

215

CCAAATGACT GTAAGCCAGA CTNGAAGCAT GTCAAAAAG

239

(2) INFORMATION FOR SEQ ID :405:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :405:

15 GGCTATTATT CTAAGTGAAG TAACTCAGGA ATGGAAAACC AAACGTTGTA 50  
TGTTCTCACT GATCATTGAG AGCTAAGCTA TGAGGACTCA AAGGCATAAG 100  
AATGATACAA TAGACTTTGG GACTTGGGAG GAAGAGCGGG ACTGGGGCGA 150  
20 GGGATAAAAAG ACTACAAATA TGTGCAGTGT TTACTGCTC 189

(2) INFORMATION FOR SEQ ID :406:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 75 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :406:

35 CACCATCCTC CAAGTAAATC CCCCTTAGG AAAGTAAGGG AAAAGACCCC 50  
TTATAGCCCT GAGCTCCCCC TTGGA 75

(2) INFORMATION FOR SEQ ID :407:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 190 base pairs

216

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :407:

|    |  |     |
|----|--|-----|
| 10 | TATTCATCCA GCAGTGTTC TCAGCTCCTA CCTCTGTGCC AGGGCAGCAT  | 50  |
|    | TTTCATATCT AAGATCAATT CCCTCTTTTA GCACAGCCTG GGGAGGGNGT | 100 |
|    | CATTGTTCTC CTCGTCCATC AGATCTCAGA GGCTCAGAGA CTGCAAGCTG | 150 |
| 15 | CTTGCCCAAG TCACACAGCT AGTGAAGCCA GAGCAGTTTC            | 190 |

(2) INFORMATION FOR SEQ ID :408:

(i) SEQUENCE CHARACTERISTICS:

|    |                            |
|----|----------------------------|
| 20 | (A) LENGTH: 194 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :408:

|    |  |     |
|----|--|-----|
| 30 | GAAGACATGG CGCCCTAACA CTCGAGACC TGCTGNTAAA TAAAAGCTA   | 50  |
|    | TTTTTCATTA AACCACCATT TCCTCCACCT ATTGGAGTCA AATATGAAAG | 100 |
|    | CTGTCGATGA AGCCTGNCTG GCTGCACAAG TTNGACTGNG TCTGAATAAG | 150 |
| 35 | CACTTTCATC ATGGACTAAG AATCCTTGGT GTGGNCNTGA TCTT       | 194 |

(2) INFORMATION FOR SEQ ID :409:

(i) SEQUENCE CHARACTERISTICS:

|    |                           |
|----|---------------------------|
| 40 | (A) LENGTH: 97 base pairs |
|    | (B) TYPE: nucleic acid    |
|    | (C) STRANDEDNESS: double  |

217

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :409:

GCAGCACAAG AGTCATCCAT GGATACAGTT CCAATCATT TAACCACTTC 50

TAAACAAGA TCATCTTCTG CAGCACCTGG TTTAGTTTA TCCTTGA 97

10

(2) INFORMATION FOR SEQ ID :410:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :410:

TTTGAGCTCC TGGACCCTTC TTTGCCTACA CTGGCCTTCC TCTCGGAGGG 50

25 ACAAGGAAGC TGGCCTCCCT TTACTCTACC NTTNNTTNTG GTCCAGGGCC 100

AGCTCTTCCG AGGCTCCAGC CTGCTTTTCG CCGGTGTCAT CAGATCATGC 150

TTTGC 155

30

(2) INFORMATION FOR SEQ ID :411:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 249 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :411:

218

.. AACGAAGNGT TCCTGAATAC CACAGCCTGC TGGGAAATGA CTAGGCGGTA 50  
AGGTTCTGCC ATGCCTGTGA CCCACCATGG ACATACTGGA CCTTAATTCC 100  
5 TCTGCTTCTG TGCTCCCTCC TGAGAACCCT TTATGAGCCT GATTCCTCAG 150  
TCTCACCAGA ATTCTGGATC ACCCAAGAGG AAAAGACTGC CAGTTCTAGA 200  
TTCCTCTATA GGGAGACCTG GATTGTTGAC CAGGTGAGAA GCCAATGGT 249  
10

(2) INFORMATION FOR SEQ ID :412:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 143 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :412:

AGAAGGAGAC AAAACACCTC CTCTGTAATA GTACCTCGAA TGGATTCAGC 50  
25 TTTACTCCTC TATAACTCAT CTTACACCN GCATATTTAA ACAAATAAC 100  
AAAATGAAAT ACTAATAGTA AAAAGGCTGA CCCATGTGGC TTT 143

(2) INFORMATION FOR SEQ ID :413:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :413:

40

GGGTCCCCC ATTCACGTAC TCCATCACAA AGTACAGGCG GTCCATGGTC 50



219

TGGAAGCAGG AGTGGAGCTG TCAGGAAGGG CGGCTTCCCG GGCAGGCCAA 100  
CACCCACTTC TCCACCATAG TGCACTCCAC GTCATCATCT GATCACAACG 150  
5 TCCTTCTTCA GGATCTTCAC AGCATAGAGC TCATCTGTGC CTTTCGTTCT 200  
GAAAGCATGA CCTTGCCAAA GCTGCCTTTC CCCAGCACCA TTAGGAAGTT 250  
AAAATC 256

10

(2) INFORMATION FOR SEQ ID :414:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :414:

TCGCAAAAGA AGNGTACCAT AACTCCTATT TCNAATGGCT GATTGTAGTA 50  
25 GCACTGGAAG TTTATCAAAA CCCAGGTGTA AATATGC 87

(2) INFORMATION FOR SEQ ID :415:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :415:

AGAGGGGGAC CAATCTAACC ATCGCTCTTC CAGTCCTACC AGCACACTCT 50  
40 TGCAGCGCCA TNCCACTCCC TGAGCTCAGG ATCCTAGCCC GCCCCCCCCG 100

220

GGATGCTAGT NNNCTCCACC CTNCCCACCT GTCATACCTG TGTANTACAC 150  
ACCCACCCGT ATCACGCAGG ACATGAACCA GCACCACTAA GGCCCCGGNG 200  
5 CAGTGTCTTG NNNTTCTTCT CTANCTGTCT GCCCTGAGTC CCGGACC 247

## (2) INFORMATION FOR SEQ ID :416:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 162 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :416:

TCTAGCACAC AGCTGCGCTC ACAAAACTG CGCGACTTGT TAGAACTAAT 50  
20 TGAGTGGAGC CTGCAGGTGA GGGGAGGGAG GGGCTGCAGG TCAGGTAAGA 100  
TCTGGAAGAC AACGCACACT TGAAGGGCAG GGGACTCTAA GCAGGGATT 150  
25 ACATTGAAAG GA 162

## (2) INFORMATION FOR SEQ ID :417:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :417:

CAGAAGAAGG AGAACTCATG ATTCCAGAGA GCTTTGGGGC TTATTTTAA 50  
40 GTACTTAGCA AAATATTGT TTNCGTGAT TTAGCTGTC ATTAAACNAA 100

221

GAGCTACTG

109

## (2) INFORMATION FOR SEQ ID :418:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :418:

15 GGATGTAAAT TATATGTTGT TTAAATTTT CCAGCATCTG AAAACCTTAT 50  
CTGCTAGACA ATGCAAGATT CACACAGAGT TATCTGGGAT TCTGATTTT 100  
TAAATAGTAC ATATCATTAA ACCATTCNTT CTAAANGTAA GAAGAGCAGA 150  
20 AAAAATCTTA TAAGATTATC AGATTTTCCT AATGACACAG AAATGNAAGA 200  
AA 202

## 25 (2) INFORMATION FOR SEQ ID :419:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :419:

TAGCAAATGT GGATTACAAG CAAATACAAC AAGTCGTGCC CCTCCAACCC 50  
ACCACAAACT TCTAAACGCC ACTCAGCAGA TGCATAGGAT TCGTTACAG 100  
40 CAACGATTGA AATAAAAATA AAAGCTNCAA ATGCAATACC CANACTAGCC 150

222

TA

152

## (2) INFORMATION FOR SEQ ID :420:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :420:

15 CAGCCCTACA CTCGCCCCGCG CCATGGCCTC TGTCTCCGAG CTCGCCTGCA 50  
TCTACTCGGC CCTCATTCTG CACACGATGA GGTGACAGTC ACGAAGGATA 100  
AGATCAATGC CCTCATTAAA GCAGCCGGTG TAAATGTTGA GCCTTTTTGG 150  
20 CCTGGCTTGT TTGCAAAGGC CCTGGCCAAC GTCAACATTG GGAGCCTCAT 200  
CTGCAATGTA GGGGCCGG 218

## 25 (2) INFORMATION FOR SEQ ID :421:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 237 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :421:

GATGCCAATG TTTCATCCAC CGGCTGCACA GGCACAACT CCCCCACCCA 50  
GGACGACTGT GATGAGGTGG CCCTCCCTGT CAACCCTGGT CCCTGGAGTC 100  
40 CCCAGCACCT GGGGCCCTGA CGGTCTCGAT GTCACAGGCG CTTACTGTGC 150

223

TGCTGGCTGT CCTATGCCAG CCTCAGCCAT GTGGGGACCA CGNAAGGCAC 200

ACTCCCTCAC CCCGGTGCCG GGCCGTGCGA TCCCCCA 237

5 (2) INFORMATION FOR SEQ ID :422:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :422:

AGGNGTAATA AATACTGCAT CCTTCCACA ACATAGCAGG AATCTTATAG 50

GGAAATCCAT ATAGTTTCTG AACATGTATT NATATACTAA GTCTATATTG 100

20 TTTCTTTACG AAGTGTAAT AAGTGCTGCA CCATACTGTA AACAAAAC TC 150

GAATATTGAC TAAATAAAT CAAAAGTTCA TCTTGTAGTC ATGTCTTTCT 200

25 CC 202

(2) INFORMATION FOR SEQ ID :423:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 216 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :423:

GGGACACCAT TACCATCCAT TGACATCGCA TTTCCATAGA AATGCCAAAG 50

40 AAAGAAGTCC TGGGGTTTTT CATAGAAAGC TCAAAAAGTT CAACCTTTGA 100

224

.. TGCTATCCCC CAGCCCAATA CAAAATACAC AAAAAAGCAA TTATCAAAAT 150  
ACTGACTTCG GTTCTTTTT CTCTTCAAAT NCCTATAATN GCTTTACATA 200  
5 TTCGTATCAG CACCTA 216

## (2) INFORMATION FOR SEQ ID :424:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :424:

CGACGAAGGG AGTACTCGCG CTTTGTCTCC CTATCCACAC TTGAGCAAAT 50  
20 GCTCGCTGGT CTACTGCCAA AACCCATTTC ACCAACCATA TGTCCCTCGC 100  
CCATACCCCC TCTCCCTCTC AAACCCTGGG GACAAATTCA AGGACCCAGG 150  
25 GGTGCCCTTT TAAAAAAA 168

## (2) INFORMATION FOR SEQ ID :425:

(i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 258 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :425:

TCGCAGGAGA AGGAGTCGCT TACTATGCAT CCAAAGGCTA CCGTGGTTAC 50  
40 TCCTATATGA CATTCCAGAT TTTGATGACT AGCACCCACC CCACAGCTGA 100

225

GAGGAGTCAC AGTGGAACCT CCCAGCTTTA AGATATCTAG CAGAACTAT 150  
AGCTGAGGAC TAAGGAATTC TGCAGCTTGC AGATGTTTAA GAAAATAATG 200  
5 GCCAGATTTT TTGGTCCTTC CCAAAGATGT TAAGTGAACC TACAGTTAGC 250  
TAATTAGG 258

## (2) INFORMATION FOR SEQ ID :426:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :426:

20

TCCACATCAT CTCCAAAGCC CATAGGCCGA GAAATGGCAT CTGAGATCTG 50  
CTGGGCCACC TCCTGTTGTT CCGTATGTCA GTCATCAGTT CATCTACCTN 100  
25 GTCAATGTCC ATGTCCTGGT AGGCCTTCTT CATGCTTTGN CAGCAAGCTC 150  
CATGCACGAA GGACTTCTGC ATTGGTAGTG GCATTCTCAA TAGCCTCAGC 200  
CTGAAACTCC AGGGTGGATA ATGCCCCGTC AATTGTGCC AGCTGCTGTT 250  
30 CGAATNNTTT TCTTTCTCGT AAAGC 275

## (2) INFORMATION FOR SEQ ID :427:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

226

## (xi) SEQUENCE DESCRIPTION: SEQ ID :427:

CTCTGTGCCT CGCTGAGGAA AAATAACTAA AATGGCAAAG AAGATCCTAA 50  
5 GAAGCCGAGA GGCAAATGT CATCATATGC ATTTNTTGGC AAAGTGTCCG 100  
GAGGAGCATA AGAAGAAGCA CCAGATGCTT AAGTCAACTN TAAGAGTTT 150  
CTAAGAGTGC TC 162

10

## (2) INFORMATION FOR SEQ ID :428:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 220 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :428:

ATGCAGAAAA GGAGTCGTGA GCGTAACACC CTCGCTGCTG GTCATAAAAC 50  
25 CCATAGTTCC TGAATCATC AAAGAACTTA ACTTCCTGAC GCCAGATATC 100  
TGCCATGCGC GAAGGGNTGA TACCACTCAG GATTATGAAT TTTGTTTAAA 150  
GTCGNGTTTA CAATGATTG NCCTGGACTG AAATTCANGC TGCCTTAAGG 200  
30 TGCTGATGAT ATTGAGAAGT 220

## (2) INFORMATION FOR SEQ ID :429:

## 35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear



227

(xi) SEQUENCE DESCRIPTION: SEQ ID :429:

5 GACTCATCTT GCCCAAGAAG AGCCAGGATA TGAGAAGATG GGAGAGGGAA 50  
GGGGAGGTGT GAAACGTGCT GGTGCTTCCT GTCCTCATGG TGTGATGGCT 100  
GCCCAGGCTG CTCCTTCGAG GCAGGACAGG ATTCCCATGG GAGATATGAG 150  
GACCATGGTG ATTCCAGGA CCAATTATGT CCAGA 185

(2) INFORMATION FOR SEQ ID :430:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 277 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :430:

GGGATGCCCT GACCTGATGG CCCTTGACCA ACATGGTGCT GGAGGAGCAC 50  
25 TACCTGGTCC TGGGAGTAGT GGTCATCGTG GACCCAGGGG TGATCCCTAT 100  
CAACTCTTGG GGTGAGAAGC AGCGCATGCA CCTGCCGGAC GCTTCCTGGC 150  
TGACCAGCTG GACCCCATCT AGTCGCCTAC AACAGCGAGC CAGCACACCG 200  
30 GCCCAGGTGC CGGAGATGAA TGAGCCCCAG CAGTCCAAGG TGTGATGTGG 250  
GAAGACACCG CAGAGCTCAC TTACCAA 277

35 (2) INFORMATION FOR SEQ ID :431:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 125 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

228

(xi) SEQUENCE DESCRIPTION: SEQ ID :431:

5 AAAGTGGCGCT TGGGCATCCT GCCAGCCTGC CATGTCTTCA TGCGCTGGTC 50  
GAAGGCAGCC NGGACTATGG CCAGGAGGCG AATGTAGTCA CTCAGGAGCT 100  
CAGCAAGGAG GAAGAAGTCA TTGTT 125

10 (2) INFORMATION FOR SEQ ID :432:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs  
(B) TYPE: nucleic acid  
15 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID :432:

GCCTAACTGT CAAAGCACAG AAAAGTTAAC AAAGGGTGGG ACTCGCCATT 50  
TCGAAATAGC ACATTTTtag CAATAGGCTC TCTACACTAG AGAGCCAGTA 100  
25 GACTGATATT CTTTAATGCC AGTTTCCTAG TTAATCGTAA AGATAGACAC 150  
AATCCCCC TTTATAAAAG CTTCTGTCGT TTCACATAAT GACTTTAACT 200  
30 ANAANGGAAA TGGGGCAGGA CA 222

(2) INFORMATION FOR SEQ ID :433:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 213 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :433:

229

CCATGNCGGC CCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT 50  
CGATTTCTTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC 100  
5 CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT 150  
TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAACTGT TGGTNTAACT 200  
NGNCGTTTCC TCT 213

10

(2) INFORMATION FOR SEQ ID :434:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 221 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :434:

CCATGNCGGC CCCAGGTCC TCGATCTTTT CGAGCTGACT TCTCATGGCT 50  
25 CGATTTCTTG GTGCTTGGTT TGGTAGCTTC AAGCTGGGAT TCGAGGGTCC 100  
CCGACTNTTC CACCATACAG GACCCATCGA GGAGGCATGT TCTGGTCTNT 150  
TGGATCCACT GGTGGAAGGG TTGCGCGCTG GNCAAACTGT TGGTNTAACT 200  
30 NGNCGTTTCC TCTGCCGGTG T 221

(2) INFORMATION FOR SEQ ID :435:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

230

(xi) SEQUENCE DESCRIPTION: SEQ ID :435:

ACACTTGATA CTATGCATCA AAGGACGTGG AGAACTAGAG CGGGCTACAT 50  
5 TAGTATATTT TCGTTGTCAG 70

(2) INFORMATION FOR SEQ ID :436:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 163 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :436:

AGTACGCAAT GCTTTCTTAC AGTAAGCAAG AGCTCCTCTG TAATCCTTCT 50  
20 CGTTGAAGGA AATGCAAGCT TTACCAAGAA GGGCTGGAAT ATTATTCGGA 100  
GACTGATTGA GTACAAAATG AACTGTGCG TCAGCTTGAT CCATTTTGTC 150  
25 ACCCTCAAGT AGG 163

(2) INFORMATION FOR SEQ ID :437:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :437:

TGTGGCTGAT CATAAGAAAG GAGCAAAGAA AGCTAGAATT GAAGAAGATA 50  
40 AGAAGAAACA GAGGACAAAA AAACAGACGT TAAGGAAGAA GATAAATCCA 100

231

AGGACAACAG TGGCGAAAAA ACAGATACCA AAGGAACCAA ATCAGAACAG 150

CTCAGCAACC CCTGAATTG 170

5 (2) INFORMATION FOR SEQ ID :438:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :438:

AGAACTACAG AAACCTGGCC TCCCTGAGTT TATCCTATGG GGGGCACAGG 50

AAAGAGCCCT GGACCATAGA AACCAAGTAC GAGTAGCAAG AAAACCAAAA 100

20 GGGTGGGAAT GGATCAAAGG TGTGAAAACA GATCTGTCTC GTAAGTGTGT 150

AATCAAGGAA CTAGCACCAC AACAGGAAGA TAACCCA 187

25 (2) INFORMATION FOR SEQ ID :439:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :439:

AAAAGCAACC AGGTTGAGA AACAAATAGTG TATGTGTTCC TATAGGTATG 50

AGTTATTCAN TGTAATTCG TTTTCTGCA ATCCTCTGCC GAAATGATNT 100

40 ACACCTACAA TGNNGAATGC CATAGGACAC TACAATCTGA ATCAAAACAG 150

232

TCGCGTCTGA AATGNTNGTG TGGTAGACCA CCCCCATTCA AGCCTTCATA 200

CTTCGTAAAA ATGCAAATGT TGAAGATCGN NTCT 234

5 (2) INFORMATION FOR SEQ ID :440:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :440:

GGACCAGGAA CCTAACTGAG ATAAGTTCAG CTTCCAGTT GACACCAAGT 50

CATCTAGTCT TCCCGGAGTA GATATAGTTG AGGTACTCCA TTTCCCAAAA 100

20 CAGAGAGCTG ATCCCGGGCT GCAACACCTC CAATAGTCGA AGCTCCCTTA 150

ATNAAGGATA TCAATGTATT TCTTAAACGC TTGATGTCGT TCAAAGTCTG 200

25 TTC 203

(2) INFORMATION FOR SEQ ID :441:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :441:

GTGATGCACC TGACATCCCC TCACAGGCTC TTGGAGAACT GTAGTGCAAC 50

40 TCACTTAACC GCAATGCTGA GAGCAGAATT CTGGAGTATG ATCCAGGGGA 100

233

ACGTTTCCCC ACACCACCCG AGCTACTTTA CCAGCGATCA TGATTGTGAT 150  
 GGAATAGGCT TATTAAGTTA CACATTTAAA AAGTCATTAG AACATCTCGT 200  
 5 TCTTGCACAC TAGTGTAGAA AGGTCTTCCA AAGATAAAAG GTGTAGGCCT 250  
 GGT 254

## (2) INFORMATION FOR SEQ ID :442:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :442:

20

GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG 50  
 CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG 100  
 25 CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGC 147

## (2) INFORMATION FOR SEQ ID :443:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :443:

40

GGGGNGCTAG CAGTTGGGNG GTGTAGGAGG CATTGCTGAT GATCTTGAGG 50  
 CTGTTGTCAT ACTNTTCANG NNNCACACTC ATGACGAACA TGGGGCATAG 100

234

CAAGGGGCGG ANGANGACCG TTTNGNTTCC TTGAAANGAG CCCCAGCTNC 150

TCCGNGNGAG ACGCAGTGGA CTNCGATGNT TAGCNCTAGT NNCCCGCT 198

5 (2) INFORMATION FOR SEQ ID :444:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 208 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :444:

ATACTACGCT AGGAGAACAA TGTTCTACA TATTATGGGT AGTGAGACAT 50

TATCTGTATA CAGGGACTGT GATTATTTAA AATATGCAGA ACTTATTTC 100

20 TCTGTGCTTT AGAAATAACT GTATACAGTG TTATAAGTGA AAGAACTCAA 150

AATAACTAAT ACCAAATATA CACCTATGTA TTAGAATTCA AAAAGCTGCT 200

25 TTCTGTGA 208

(2) INFORMATION FOR SEQ ID :445:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :445:

AGCACATTTT ACTACGGGNT ATGTGCATTC TGGGCTTAGT AATGTCAAAT 50

40 CACTCTTCTC TCCAGCTTGG CCATTCCTCA TTCCTGCGG GCCTGCCCTG 100



235

TAGACCACAG GCTAATGGAA TGTCCCGGTC TGNGTCATCA NATTCTGTAA 150  
CCTGNAGCCC CCGCTGAG 168

5 (2) INFORMATION FOR SEQ ID :446:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :446:

AGGCAGAAGG GACGCTACTG ACTTAAGCCA AACCCCTGATT GGTGGATAAA 50  
GTATTCAGTT GTTCCATTCA TGCCTATCCT TTNTACAGCT CTCGCGACTA 100  
20 TAACAAACAA CTGATAAAAT AGCATCAGTC CCTCCACCAG GTTGCCCTCA 150  
AGGAAGCCAT GTTTGTGACG ATCCGACCAG TCCCTGACGA TCTCTCTAGA 200  
25 CCACCCTGAC CTCGCCGAGA GTGCTGAAGG AGCTATCTAA CCA 243

(2) INFORMATION FOR SEQ ID :447:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 251 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :447:

CAGTCAGGGT CACAGAACAG TATTCAAAT GATTGCCAC CTGTTTTAGA 50  
40 AATCTAAAT NNTAAGTAAC TAAGAGCAA GTGCTATGTG GGTTTTAGAC 100

236

CATGACTGTT TGTTTGCTCT CCTGCCCTAC CACCAAGCAA AGCAGCAGGG 150  
CTCCTGGGGG AGAGGGATT CAACCCCCCT GATGGCAGGG GGTGCTCTGG 200  
5 GGAGGAGAGA GGAGAGAACA GGCTGTTTTG GAAAATATCC AGCACTTTGA 250  
C 251

## (2) INFORMATION FOR SEQ ID :448:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :448:

20

ACACTCCAGA NCATCCCACT AGAAAAACAA TTNNCAGGA ACGTGATGGC 50  
AACAATCAGC AGCCAATATT CTCAAGAGTT CCTAATCACC AAAAACATAT 100  
25 ACAATNTAGT CTAGAAAAAT AAGTCAATTT CATAAAATAA GTTTTATAGT 150  
CGAAAAGCAC CCCCTTCACA GGTACAGAGA TACTGAAAAA TAGTCCCTAA 200  
AAATCTACTC ATAGTTTACG GAGAGAAAGG CATGCCATGT GAGTTACGGA 250  
30 GTG 253

## (2) INFORMATION FOR SEQ ID :449:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

237

(xi) SEQUENCE DESCRIPTION: SEQ ID :449:

ATATAAAAAA GATCCGCATA ATAAACCAAA TCAGAAAATA ATACCTTGTA 50  
5 ATACCTCTGT AAGAAGCAGA ATACACCATA TGTTATTCAC ATGTATAGGA 100  
GTGATAAGAA AAT 113

(2) INFORMATION FOR SEQ ID :450:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 211 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :450:

20

TAGCATCCAG GGGAAGTTAA TCAATACGCG AAAAATACTG AAATTAAAGA 50  
GACAAGTAGA AGAAAATGAA ATAATCAAGA GATTGAGAAA AGTTGCCAGA 100  
25 AAGCTTGGAG AAAAACCAAG ATATGTAATT TTCGCAGAAG TCAAAGGTAG 150  
AAACTATTTG AGATCAAAGT CCTATAAACA AAGTTAAATG ATTCCAAGAG 200  
GTAAATAGGA G 211

30

(2) INFORMATION FOR SEQ ID :451:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :451:

238

CTCCATTAGC TTTATGGGAC ATACGACGCA TAAAGATACT NTCCCGTGCG 50  
NATTTACAC NTGNCAGAGC TATAAACCGG TGNATGATGT GATTTNCTG 100  
5 TAGAATGATA TGGCCTGATA TGGAGGCCTC TTAATNGGCT TTTCAAGCA 150  
GCAAAATGGT CTTGNGTGAG TCGTGCCGAG GCTNNNGATC AAAG 194

## (2) INFORMATION FOR SEQ ID :452:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :452:

20

ACTTCAAGCT CAACCTATTC TCGTCTCTT TGTTAGAGGT GTATTGAGGA 50  
TAGCATATTG AGAATATATT CTCTGGTTCA AACCAAAGAT TTTGTGACAT 100  
25 TAAAACTACT TGAATTTCTA CTTCATAATA GGAGTCAGTC ACTTCTGGGA 150  
CTATAGTGAT GCTTGCAA 168

## (2) INFORMATION FOR SEQ ID :453:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :453:

40

CGATTCTTGC CCTAGTCAGA GACTATAGCA GCCCCAGAC GTGAACCAAT 50

239

TGGCCATCTC CAGAAAGTTT AACAAAACCC GACCAGGTTG CCCCCTTCAC 100  
TTTCTTACAA CCTCTTCCCC TTCCCCAGGG GCTCTGCTCC TCACTCCAGA 150  
5 TCATCCTTTA GTTTAGAGCT GCGCAGTGAA GTGGATATCA CTGAAGGAGA 200  
TAGGACGCCA GACTACACTG 220

## (2) INFORMATION FOR SEQ ID :454:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :454:

20

GCCATCCTTG ATGGAAAAGA AACTGAAGAG AAAAGACAGC CTGTGGAAGA 50  
AGCTCAAAGG TTCTTTGAAG AAGAAGAGAG AAAATATGAC ATGATATCTT 100  
25 TGCTTTTGAG TTCCTCACGC TCTCTGAATN TTATTGGTTG GACATTCCAT 150  
ATGTAGCATT CTGCTTCAAT ATTATCTATT ATGTGTCTCT CTCTCTTCAA 200  
ATANNITGCCT GTAGGTAAAA GCAAGCTCTG CATATCTGTA CCTCTNGAGA 250  
30 TAGTTTGTCT TTGTCTTTAG CGGTT 275

## (2) INFORMATION FOR SEQ ID :455:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

240

## (xi) SEQUENCE DESCRIPTION: SEQ ID :455:

TCGCAGAAGG AGGAACGGGG ACTTTCATC CCCTGAACCA AGGCATGTTA 50  
5 ACACTTGGCT CCAGCATGTT GTCATCATTC AACCAGAAAT CGCACAAATG 100  
CTACTGTGCC GGGGTGNAGC CAATTTTCTT AAGTAAGTGC TGAATTCCTT 150  
AACANNTATC TNTNTTNTGG CTGTAGGGTG GCTCAGTGA ATCCATTTTG 200  
10 TTAACACCGA CAATTAGTTG TTTCACACCC AGTGGTAAGC CAGAAGGGCA 250  
TGCTCTNGGG TCTGCCCATT 270

## 15 (2) INFORMATION FOR SEQ ID :456:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :456:

TCGCAGGAGA AGGAACCTTG ATGATACCAT TATCCTCACT TAGATGATGC 50  
ACGACCCCTG CGCTGGATAC GCGACGGTT TCTCATTTCG CCTTGCCAG 100  
30 CTCTCATTTCG CTGAGGGGCA TAGACCTTTT GATATCATCC AGGCTTTAGT 150  
TTCTTAAGGA GCAAAACAGC TTCCTTGNNC TTCTTGTAGC CTCAACTTA 200  
35 TTAAACTAC CAAGGAAGTT CAGGAAGTTC CTCAANACGA TGACCTTTAG 250  
ACAT 254

## (2) INFORMATION FOR SEQ ID :457:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 base pairs

241

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :457:

|  |     |
|--|-----|
| ACACTAACTG TTCCATCCGT TATATTGCT GTGAGGAAAA TTAAGATTCC  | 50  |
| TGTTGTATGG GCTGCACTGT TTCTGGAAGA CTACAGAAAA TCTAACATGG | 100 |
| TTGACACTTC CTGGTAGCCC TTCTGTACAT ACACACACAC AACCAAGAGA | 150 |
| GAAGACAGAG AGAAAATCCT GGTCCAAAAG ATCACATGAC CTTACTAGTG | 200 |
| TTTCCCCAAT GACTGTAATT TATAAACTAA AAATTG                | 236 |

20

(2) INFORMATION FOR SEQ ID :458:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :458:

30

|  |     |
|--|-----|
| GAGANNNNTT NNGGNAAATG NTTNCGCACT GNAGCTAAGA ANAGNNATGG | 50  |
| NNNTAGGGNG NNAGANGNCN TGAACAGAGA AAGCNTGAGG GCTCTGGGAC | 100 |
| GCTGGTAT   | 108 |

35

(2) INFORMATION FOR SEQ ID :459:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

40

242

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :459:

ACCCATGGCA AATAGGAAGA AGCTCAGTAT CGGCTCCTCC CACCATAACC 50  
CCCACTTCTC CCGCCTCCTG GACCATAGTT TCCTCCACCA TACGGTCCCC 100  
10 CCATGTTCTT GCTACCACCA AAGTTTCCAC TCTCCATTGG ACCGTAGTTA 150  
GAGGT 155

15 (2) INFORMATION FOR SEQ ID :460:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :460:

TGCTATTTCC CTTTCATAAA GGCACACATT TGATCTTATC TTCTCTTACC 50  
CAACACGCAG TGGCAGTGTG TATTTTCCTT CTCTTTTTTT GTTAAATATT 100  
30 CTGGTTTGTG GAGGTTTACA GACATGTGTT AGTATATCCT TGCCTGCATG 150  
TAGTTGTTCA TTACTAGAC 169

35 (2) INFORMATION FOR SEQ ID :461:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



243

## (xi) SEQUENCE DESCRIPTION: SEQ ID :461:

5 ACCNTGTTTA ATTANTGCGC GGGCTCGCCG TTTGCATACA ATGGCTTACT 50  
CAGTGCTNNC AGGCTGTGAG TNAATAGAGN GTGTATGACT TAATAAGCAT 100  
TTTATCAGCG TACCTTTTTTC GCCATGCGCT ACCTGCTATT GATGAAGGCG 150  
10 GCTTAGGGCA TCGAAAAACC TAAAAGTCGA GCTT 184

## (2) INFORMATION FOR SEQ ID :462:

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 275 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :462:

25 AGGAACCN TG TTTAATTANT GCGCGGGCTC GCCGTTTGCA TACAATGGCT 50  
TACTCAGTGC TNNCAGGCTG TGAGTNAATA GAGNGTGTAT GACTTAATAA 100  
GCATTTTATC AGCGTACCTT TTTCGCCATG CGCTACCTGC TATTGATGAA 150  
30 GGCGGCTTAG GGCATCGAAA AACCTAAAAG TCGAGCTTNG NNGTGCCGGN 200  
AACGGCTCTA NANTACTTCT CATTGTAACT AGAGTACCAT ATTCGGCCGT 250  
NNACTGNGTT GTTGGCGACA GATGT 275

35

## (2) INFORMATION FOR SEQ ID :463:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 149 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

244

(xi) SEQUENCE DESCRIPTION: SEQ ID :463:

5      AATTCACTAT GCGTGGCCGC CACAGCTATN CTTGTCCTCC TGGATCCTGA      50  
ACCTTGNAAG CTGCACTAAT GAGTTCAACG GGAGTGCTCT GGGCCCAGGT      100  
GTCAGCTGTA GCAATGCCCC NGCTGCAACT GAAGGNGCCA GCAATGCTA      149

10

(2) INFORMATION FOR SEQ ID :464;

(i) SEQUENCE CHARACTERISTICS:

15      (A) LENGTH: 179 base pairs  
         (B) TYPE: nucleic acid  
         (C) STRANDEDNESS: double  
         (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :464:

ATCATCAGCA GTGTTGCTCA GCTCCTACCT CTGTGCCAGG GCAGCATTTT      50  
25      CATATCCAAG ATCAATTCCC TCTCTCAGCA CAGCCTGGGA GGGGGTCATT      100  
GTTCTCCTCG TCCATCAGAT CTCAGAGGCT CAGAGACTGC AAGCTGCTTG      150  
CCCAAGTCAC ACAGCTAGTG AAGACCAGA      179

30

(2) INFORMATION FOR SEQ ID :465:

(i) SEQUENCE CHARACTERISTICS:

35      (A) LENGTH: 156 base pairs  
         (B) TYPE: nucleic acid  
         (C) STRANDEDNESS: double  
         (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :465:

245

CTACCTCTGT GCCAGGGCAG CATTTTCATA TCCAAGATCA ATTCCCTCTC 50  
TCAGCACAGC CTGGGAGGGG GTCATTGTTC TCCTCGTCCA TCAGATCTCA 100  
5 GAGGCTCAGA GACTGCAAGC TGCTTGCCCA AGTCACACAG CTAGTGAAGA 150  
CCAGAG 156

## (2) INFORMATION FOR SEQ ID :466:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :466:

20

ACATCCCTGG AAGGAGGGCC TGAGGGCCAG GGAGGGAACA AGGCAGGAGA 50  
CTGCTGGTTC TGGTTTTGGC CACCTCACCC TTGGCCACGT CCCCTCCGGC 100  
25 TAAGCCACAG CACAAAGCAG AGCCAGGCTC TGGAGGCCCA GGGCCTCACC 150  
ACTCCCCTNT GTCCCCCAG CAGGGGGACA AAACAG 186

## (2) INFORMATION FOR SEQ ID :467:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :467:

40

TNNNGATGAN TATANAAGCA TCATNGACGG TATTCCCNG TCTTGNANTT 50

246

TNATCGAGAN TTTANTCTAG TAANTATATT AATNTNT

87

## (2) INFORMATION FOR SEQ ID :468:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 187 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :468:

15 ACTAGAAGTA CAGCATCCTG CTGCAAAAAT GATTGTAATG GCTTCTCATA 50  
TGCAAGAGCA AGAAGCCGAG ATGACACAAA CTTTGCCTGG TATTTGTTGG 100  
AGCTCTCCTG GAATCACTGA AGAACTTCTG AGGATCGGCC TGTCAGTTTT 150  
20 AGAGGTCATA GAAGGTCATG AAATAGCCTG CAGAAAA 187

## (2) INFORMATION FOR SEQ ID :469:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :469:

35 AGGGCACCAT TACCATCCAT CTGACATCGC ATTTCCATAG AAATGCCAAA 50  
GAAAGAAGGT CCTGGGGTTT TTCATAGAAA GCTCAAAAAG TTCAACCTTT 100  
GATGCTATCC CCCAGCCCAA TACAAAATAC ACAGAAAAAG CAATTATTAA 150  
40 ACATCGGCTT CGTTTCTTTT TCNCCTTTGA ATNTTAATGT TTACATACTA 200

247

GTGTGCAGCA CCTACTTCTT NATCGCCGTG AACTGAAATC TAGATTTTAA 250

ACTGAA 256

5 (2) INFORMATION FOR SEQ ID :470:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :470:

CTCAAAACGA CAATTCTGTG CCTGGGGGAT CTGACCTGGT GAGGTAGCCT 50

GAAGTCTGAA TGGAGCCCAT AGTCGAAAC AACCTAAGAA TCTCTCAGAA 100

20 GAGGGTTTG 109

(2) INFORMATION FOR SEQ ID :471:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 139 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :471:

35 GCGGCAGTAT ACAGAAGCCA TATCAGTTGG GAAAACTTT ATCAATCATA 50

GAGCCTTTTG AAGAAAAATT TGCCAAGCGT GGTTTTTTGC TTGNAGACCT 100

40 ATATATATTA CCTACAGGCT GAGAAAGCTT TGNATTTCT 139

(2) INFORMATION FOR SEQ ID :472:

248

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :472:

10

|  |     |
|--|-----|
| TCGCAGGAGA AGGAATGTTC CCAATAGGAA CGCCTGTAGA CTGTTCAGAA | 50  |
| GAAATGCCCA AATGAGCCAG ATGAGAAGGC TGAGGGCAGG GCTGCTTTTG | 100 |
| GCTCTGAGGA CTATAGATT ATCCTCTAGG TGATGAGGGA CTATTAACGG  | 150 |
| CTGGTGAGTC TGGAGAACTG AACAGTGGAA GCTCTATTTT AGATTCACGT | 200 |
| GGCAGTAGAG GATAGAGGTG TTTGGAAGCG GTGGGCAGTT GCAAGCTATA | 250 |
| TGGGAGACAT TT  | 262 |

20

## (2) INFORMATION FOR SEQ ID :473:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :473:

35

|  |     |
|--|-----|
| ACAGAAGGAC TTTGTCTCTT TAGCTTGTTT AGCTCAATGA ACATTATCTC | 50  |
| GGCAAATGAC TCTGCTTTCT CGAAGGTCCT TCTCCGCTCC AGGTTTACTT | 100 |
| GCATCTCTCA TACTTNNTAC AGCCAACATG AACACTCTAT GTATTTTCTA | 150 |
| AGCTTTCNTC TGTTCAGAA CTTTGAATTT AAAACGTCT              | 189 |

40

## (2) INFORMATION FOR SEQ ID :474:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 166 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :474:

TNCGTGCCTA GCAAACCTAA ACTCGAACGC ACGTAATAGT GCTCATAATT 50  
15 CTNTNAAGGA CTTTAAACTT TACTCNGTAT GCTNTNTTGA TGACTCTAGC 100  
AGCCTCGCTA ACCTAGTTTA CCCCACTGTC CCCACCGGCG AACTNTTTGT 150  
GTTAGTACGC GNGTTA 166

20

## (2) INFORMATION FOR SEQ ID :475:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 109 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :475:

TTTTTTTTTA GTAACACTAA AGAGCTGTAA AGAACATTGA AGGTGGTCAT 50  
35 TCCTTCAAAA CTGTGTTTTG ACCACACAAG GTGGGCATTA ACAAACAAAT 100  
TCAACTTAA 109

40

## (2) INFORMATION FOR SEQ ID :476:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 base pairs

250

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :476:

10 TCTGGGCGGA AGGTGGTGCG GTGAAAGGTG CAGGGACAGA CTGGGTTAGA 50  
GGCCACTCTT GGTCTTATCC TCCATGGCCA CAACAGAGGT GACAAATACA 100  
CGGGTCACTC AGTTACGTTT AGCCACAGCC T 131

15 (2) INFORMATION FOR SEQ ID :477:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 265 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :477:

ACATGGATAG GTGTATGCAT ACTACGGCTA AGGAGAAACA ATGTTCTTAC 50  
ATATATGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT 100  
30 TAAAAATATG CAGAACTTAT TTCATCTGTG CTTTAGAAAT AACTGTATAC 150  
AGTGTTATAA GTTGAAAAGA ACTCAAATA ACTAATACAA ATATACACTA 200  
35 CGTATTAGAA TTCAAAAAG CTGCTTTCTG TGAAGTCAAT CAGCTATATT 250  
AAAAAAGACA CAAAT 265

(2) INFORMATION FOR SEQ ID :478:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 182 base pairs



251

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :478:

|    |  |     |
|----|--|-----|
| 10 | AATCTACCAA CCTTAAAGCT CCCGNGATAA AGCTGTATTT CCAAAAGACC | 50  |
|    | TGTNTTTATT NGNNGGNGTT NGCTTTCTTT GTCATCTAGA GCCTTGTTGT | 100 |
|    | ACATGCAATG GGTGGGAGAT AGTGGTACCT ACTGTTGNTT CTNTCTGTGT | 150 |
| 15 | NTTCATCATG GTGTTGTCTA GGTCTCCTGA GG                    | 182 |

## (2) INFORMATION FOR SEQ ID :479:

## (i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 20 | (A) LENGTH: 169 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :479:

|    |  |     |
|----|--|-----|
| 30 | AAGCCGTCGG GAGCCGCCGC CGCCATCTGA GGGAGGTACC CTGGAACCA  | 50  |
|    | CCTTTCACGG TGGGGAAGTG CAGTCGCGGT GGGCAGCTCT GGGGCCACGA | 100 |
|    | AACGGGAGCC TCTAAATCTT GGTGGGACT GCTCGCCTGG AGCCGCACTC  | 150 |
| 35 | TTGAGTCCGA GGCCATCTT                                   | 169 |

## (2) INFORMATION FOR SEQ ID :480:

## (i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 40 | (A) LENGTH: 238 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |

252

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :480:

AGATAACGCT CCCATCCCAG GCTAGAGACT CCATCTCTAA TTTNCNCAST 50  
CCGTCAATGA GAGGCAGGGA CTGAAATCCC AAGTCTGTG TCACCGGATA 100  
10 TTTTCCAGGA ATGCCTCTCT TCCAAACATC AGCGACATT AACAGACCCCT 150  
GAGCAGCAAA CTTCTGCCCC AGAGGAAAGC AGAAAACCAA TTTATGTAAA 200  
15 ATTAGAAGCG ATTTGCTTGA TCCATCACTN GCTTCCAC 238

(2) INFORMATION FOR SEQ ID :481:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :481:

TCGCAGGAGA AGAAATCAAC CCCTGCTTCT CAAATCCAGA CAGGCCACAC 50  
30 TGGCTAGAAC TTCCACCCAG CAGTCCTGCT CCTGCCCCGAA GTCTGCAAGC 100  
AAGTGAACCA CATGTCGCTA TGAAAGCACA CAGACAACAG ATTAGGGCAG 150  
35 ACCTGGCAAA GATATGCCTG TCTGCCATCT TGGCCCCTGT CTGAGGGAGG 200  
C 201

(2) INFORMATION FOR SEQ ID :482:

40

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 162 base pairs

253

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :482:

CGGCTCAGNC TGTGGCGCG AAGAGAGTCT AACCCAAAAT TGCAAAAC TC 50  
10 CCGTTGATTT CCAGGCCCTA CCACACGGCG ATGTCAACTT GTCCTCCAGA 100  
CATGGACGAC TACCAAAGAT CCCAGCTACG AAGCATGGCC TTGCTTAGAA 150  
15 ACNTTTTTTAG AT 162

(2) INFORMATION FOR SEQ ID :483:

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :483:

ATATGAAGGA GGAAATGCTC GTCACCTTCG TGAATACCAA GACCTGCTCA 50  
30 ATGTTAAGAT GACCCTTGAC ATGAGATTGC CACCTACAGA AGCTGCTGGA 100  
AGGCGAGGAG AGCAGGATTT CTCTGCCTCT TCAAATCNC NTCTGAACCT 150  
35 GAGGGAAACT TTGGATTCTC CCTCTGGTCG ATACCCACTC AAAAAGGACA 200  
CTTTTGATTA GGACGGTTGA AACTAGAGAT GAACGGTTAT CAACGAAACT 250

(2) INFORMATION FOR SEQ ID :484:

40

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 132 base pairs

254

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :484:

10 AACATTATCT TGACAACTG AAGAACACTT CAGTTAACAC TACCTCGAAG 50  
AACCATCAAT GACTTGCTTT GAACAGACTA TAAAAGGCAT TCTCAAGGAG 100  
ATTAGAATGT TAATGCCACT TTGATTAGAT CT 132

15 (2) INFORMATION FOR SEQ ID :485:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 129 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :485:

TGTGCGTGGA GACGGTGGAG AGTGGAGCCA TGACCAAGGA CCTGGCGGGC 50  
CGCATTACAG GCCTCAGCAA TGTGAAGCTG AACGAGCACT TCTTGAACCC 100  
30 ACGGACTTCT CGACACCATC AAGAGCGAC 129

(2) INFORMATION FOR SEQ ID :486:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

255

## (xi) SEQUENCE DESCRIPTION: SEQ ID :486:

TCGCAAGAGG AGACATTCTG ATCATCCTCA CTGGACGCCA CAGGGGCAAG 50  
5 AGGGTGGTTT TCCTGAAGCA GCTGGCTAGT GGCTTATTAC TTGTGACTGG 100  
ACCTCTGGTC TCAATCGAGT TCCTCTACGA AGAACACACC AGAAATTTGT 150  
CATTGCACTT CAACCATATC GA 172

10

## (2) INFORMATION FOR SEQ ID :487:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :487:

ATGCTGCACA CTATGTCTCA CAAACTAAAT GGATCCATTA AAAGTTATGA 50  
25 TTAAAAGGC GACCACCCCC AAAAGAAGTC ATAACACTCA AGGGTGTCAA 100  
TATATACAAC TGTGTAAACA CAACCAATCT ACAACTATAT CAACACAACC 150  
AGCACTCCTC TATGGGCACA GACACACACA CAAAATTGTC CTTGCTTTTC 200  
30 TCAGATATAT 210

## (2) INFORMATION FOR SEQ ID :488:

## 35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

256

(xi) SEQUENCE DESCRIPTION: SEQ ID :488:

ACATGGATAG GCGTATGCAT ACTACACTAA GGAGAAACAA TGGTCTACAC 50  
5 ANACGTTAGTG AGAACATTAT CTGTATACGG GAACTGTGAT 90

(2) INFORMATION FOR SEQ ID :489:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 99 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :489:

ACCATGAGAC CTACATCCGA ATCTGACCCA GGCAAACATA CCGGGAGCCA 50  
20 TACCGCACTA NCGGCTCTTC TCAAATCTCC TGGCCACNCA CCGAGNGCC 99

(2) INFORMATION FOR SEQ ID :490:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 186 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :490:

35 GGAAACCTGG AGGTGCGCAT CCTCCAGTGC GAAGAGAAGG TCTTCCCCAG 50  
CCCCCTCTGG ACTCCATGCA CCAAGGTCAT GGCCAGGAGC TCTTGGCAGC 100  
TCAGCCCTGC CGCCCCAGAG CATGTGGCGG CTGCTCTCTA CCAGCCGAGA 150  
40 GCTTCGGAGA TGCAGCATCT GCGGCGAATG CCCC GA 186

257

## (2) INFORMATION FOR SEQ ID :491:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :491:

AGCCAACTAA GTTCTCTCTT CGTGAACAC AGGTCCATGA GTCGACACAA 50  
ACACTAATGC AAGAACCATC ACGGAAAACC ACCGCAGCAG CTGAAACTTT 100  
TATAGCCCAT AAAAGGACCA AACAAGTAAG CTGAATGACT GTGAAAATAT 150  
GACCTTCCAG AGCGGCACAT AACAGGATAT CAAATCAGGC TGATGCTTAG 200  
CAGGCTTCAA ATATNATGGT CAAATGACTG GATTACTTAN ATGAGGCAAC 250  
TTCATATCGG AAA 263

25

## (2) INFORMATION FOR SEQ ID :492:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :492:

AGAGTGGGGT TAGCTCTGCC TAGCGCTACA CAAGAAAACC TCCCTCCAGT 50  
AAATNGGTGT GGGNGGTCCG CTTTGGCCA TCATCGCACC CCCCCTGCA 100  
CTGGGCGTTG TTGCCGGGCA CTGTTTNNC NGGCTGGGTG TGTACCGTAA 150

40

258

CCGTGGGTC

159

## (2) INFORMATION FOR SEQ ID :493:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :493:

15 GGGCAGAGNA AGAACTGTTC CACCAGGTGA ACAGTCCTAC CTGCTTGTA 50  
CCATAGTCCC TCAATAAGAT TCAGAGGAAG AAGCTTATGA AACTGAAAAT 100  
CAAATCAAGG TATCGGGAAG AATAATTTC CCTCGATTCC ACAGGAGGGA 150  
20 AGACCACACA ATATGTNGTG CTGGGGCTCC CCAAGGCCCT GCCACCT 197

## (2) INFORMATION FOR SEQ ID :494:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :494:

35 GATGGGGAAG GGCATCCCAA CACAGCCTGT GGATCCTGGG GCATCTGGAA 50  
GGGCGCACCA TCAGCAGCCT CACCAGCTGT GAGCCTGCTA TCGGGCCTGC 100  
CCCTCCAATA AAAGTGTGAG AACTCCACTG TGTGCCCTGT CTTTGGGCAG 150  
40 GGAGGGCTGC TGTGAGTGGA GTCTTGAGTN GGTGAGTG 188



259

## (2) INFORMATION FOR SEQ ID :495:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 169 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :495:

ACATGACCAT CCGCATCCGC CTTTATTGAC AATGAGAAGA TGGAGTCCCG 50  
GACGCATCTA TCCCTCTTTG GCCCTTACAG GTTGCCACG AGACTGAGAC 100  
GCCTTCCTGG ACCAGGGGAG GGNGNGTTGG TNCTNTGNGC GTGNGGGTNT 150  
GTGGGNGCTG CTGGGGAGG 169

## (2) INFORMATION FOR SEQ ID :496:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :496:

CAGAGAGAAC GTTCTATGG CTGCTGCTTC TAGGAGTCTC TCGCTCATAG 50  
AAAAGGCACA CACTGAAAGA GGAAGCAGAT CCCATTGCTG TGGAAGTCCC 100  
ATTGTTAGGA AGCTCTGCTT TTCTGGAGTT CAAATTCGCA TTCATGATGC 150  
TTTAAACCGT CAAGCTGGGT GG 172

## (2) INFORMATION FOR SEQ ID :497:

260

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 246 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :497:

10

GAGAGTGGGG TTAGCTCTGC CTAGCGCTAC ACAAGAAAC CTCCCTCCAG 50  
TAAATNGGTG TGGGNGGTCC GCTTTTGGCC ATCATCGCAC CCCCCGGTC 100  
ACTGGGCGTT GTTGCCGGGC ACTTGTTTNN CNGGCTGGGT GTGTACCGTA 150  
ACCGTGGGTC CTCTGACAAG TGCCTAACTC GGCCACCCC TTAGGGTGTG 200  
TNTCATCGAA GTGTAGNGAA TGGTGAACG TTTGTTTGTN GTGTGC 246

20

## (2) INFORMATION FOR SEQ ID :498:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :498:

GGCCCTTTAC CAGCAAGTCC TCTACTCAGA AAGAACTGAC CCACGCAAGT 50  
CTGGGAGAGT GACTAGTTCA AATGTGCAGG GCTGAAGCTT CCAAACACAG 100  
CCACTATTTT TGTTGTATAT CTTCATCTCA ATGGCGACAT GGCCACTGCC 150  
CAAGGAACTT GTGGCAGGGA TCCCAAGGTG AGGCAGCAAC AGATGTCTGT 200  
GAACATCGTG CGTTA 215

40

261

## (2) INFORMATION FOR SEQ ID :499:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :499:

GATNGCCACA TCTCAACACT ATACNACTCG CTNTTCGAAT TCGCCGTNTT 50  
AGAACCGCAA GAGACCTTGA TTTAGTCACG CGAGTTCGTC TTCCTGTTCC 100  
ACANGAAAAT AAAGCTAGGG AGGTGATTTA TCTATCCGAG AAAAAAGCCG 150  
GGGACTGGTG GAANNNGAAC AATGNTCTCT NTGTCGTACT ACAAT 195

20

## (2) INFORMATION FOR SEQ ID :500:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :500:

GCGGCCTTGG GGGCACCGGC GTGTCCTGCC CAGTGGGATT AAAAAATAAT 50  
GCTCCCCACA TGGCGGGCCT TTGAGGTTC AGTAAAAATG CTTTCAACAA 100  
ATGGGCAATG CTTGTGTGAT TCACAATCGT GGCATTTAAA GTGCACAAAG 150  
TACAAAGGAA TTTATACAGA TTGGTTTACC GAAGTATAAT CTATAGGAGG 200  
CGCGATGGCA AGTTGATAAA ATGTGACTTA TCTCCTAATA AGTATGGGGG 250

40

262

GTGGAGCTGT

260

## (2) INFORMATION FOR SEQ ID :501:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :501:

15 AAAGGCATAG TAAAAATAAA ATCTACGTAA GTAACAATCT AATACTATAT 50  
TAAATNCGTT GCTACAAAGT GTTTTGTTTC TCTAAAAAGT AGTTTTTGCA 100  
TATCATTCGA CCTCTTCACC CATNTGCTGG CTTATTGCT TTATATACAA 150  
20 CAGTTAAAT TTGTGCACTA AGCTGAGCTG CCTTCACAAT GTGGTTCAGA 200  
CAAAATGCAC CCAAAGAACT ACATGTTAAG AGAGTTTATG TCCATGCTCA 250  
25 ACCATGGCTT GCCCAAAT 268

## (2) INFORMATION FOR SEQ ID :502:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :502:

AAAACTCTA ATCCAGACTA CAGTTGTCGA GATTCAAGTC GTGAGTGCAG 50  
40 GAGCGTACAC AGTGCCGTGC TGGCACATGC ACTGCACACG CTCTAGAGAC 100

263

GCTGACCTGG CTCTCGGAAA CGCAGGAGTC TTTCTGAGCC AGCTCAGAAA 150

CC 152

5 (2) INFORMATION FOR SEQ ID :503:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :503:

CCCTGACCCC TCCTCACCAC CGCGCTGCAC CTCAGGGTTA CAAGAAGAAC 50

TAGGAAATAA CGCCGGCCAC CNGACCCCTG GAGAGGGGCC GGCTAGAACA 100

20 NTTCTAAGAT CCNGCACAGC AGGTCCCGNA TGTNGAACCT T 141

(2) INFORMATION FOR SEQ ID :504:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :504:

35 CACACGACAC ACGACACGCA CGCAAACACG CCAGACGCGA CAGAGCGCGC 50

GCGGGAGCGG AGCAGCGGAA GCGCAGCAGC GCACACGAGA GATAAGGGCG 100

GCCGAGC 107

40

(2) INFORMATION FOR SEQ ID :505:

264

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 193 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :505:

10

ACCCTCTTCT GATAAATTG AGGGCCCGTT TGTCCTTGGG GACCTTCAGT 50  
AACTCCATGG CGCGCCATCG TACGGGGCAA ANACACACCT CCCGAATCAT 100  
GTCCCGCACG AACTTGGTGT GTTTGGTCAG ACGCCCGCGT TNGGCNTGTG 150  
CTGGGCTTGC TCACGTTCTT GTCACCTTGT GGCCCTTGTT GAG 193

## (2) INFORMATION FOR SEQ ID :506:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :506:

30

ACATGGATAG GCGTATGCAT ACTACGCTAA GGAGAAACAA TGTTCCTACA 50  
TATTACGGGT AGTGAGAACA TTATCTGTAT AACAGGGAAC TGTGATTATT 100  
TAAAAATAGC AGAACTTATT ANCTGTGCTT TAGAAATAAC TGTATACAGT 150  
GTTATAAGTT GAAAAGAACT CAAAATAACT AATAAATATA ACCTATGTAT 200  
TAGAATTAAA AAAGCTGCTT TCTGTGAAGT CAATCAGCTA TATTAAAAAA 250  
TGACACAAAT CCAAACAAGA TGCA 274

40

265

## (2) INFORMATION FOR SEQ ID :507:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :507:

CAGGAGAAGG AAGGTTGTAC GTGGACACTA TAAAGGTCAG CAAATTGCAA 50  
AGTAGTCCAG GTTTACAGGA AGAAATATGT TATCTACATC GAACGGGGCA 100  
GCGGGAAAAG GCTAATGGCA CAACTGTCCA CGTAGGCATT CACCCCAGCA 150  
AGTGTTTATC ACTAGGCTAA AACTGACAAA GACCGCAAAA AAACCTTCAA 200  
CNGAAAGCCA AATGTNCCAG CCGGAAAGGA AAGNGCATAC AAGGAAGAAA 250  
CCATTGAGAA GATGCAGGAG TAAAGTATTA T 281

## 25 (2) INFORMATION FOR SEQ ID :508:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 180 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :508:

AGGGNTGCTA ANNTATTGGT GGGCAGGAGG CATCGCTGAT GATCTTGAGG 50  
CTGTTGTCAT ACTTCTCATG GTTCACACCC ATGACGAACA TGAGGCATCA 100  
GCAGAGGGGA CAGAGATGAT GACCCTTTCG CTCCCCCCTG CAAATGAGCC 150

40

266

CCAGCCTTCT CCATGGTGGT GAAGACGCCA

180

(2) INFORMATION FOR SEQ ID :509:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :509:

15 AAATGCAAAA CTCACCGTGC AACTCCTAG ATCCCTGCCA CAAAGAAATC 50  
TTTGAAAAAT GAAGTCTTCC TTTCGGACAA TATACCATTN GAGTTTCTCT 100  
ATTT 104

20

(2) INFORMATION FOR SEQ ID :510:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 171 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :510:

GTNNATACAC AACTAAGTTC AAATAAAAAA ACCAAATNAA AAATNGGCAG 50  
35 GGAAGCTAGA GCCAGAATCA GGAAAATCTG TTTCCTCGTC CCCAGACTCC 100  
CGCCAAGCCT ACTCCACTAA CTAACANNGA CTCTATCAAG TTTCTATCAA 150  
GACTTGCATC TGNATCTTGN A 171

40

(2) INFORMATION FOR SEQ ID :511:



267

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :511:

10

ACTGTACCTA TCATCCTGAA AAACCTTATG GGGGAGAAAG GTCAGCAGCT 50  
TCTCTTTCTT TTNATCGAAA ATAATAAAAC TGCCTATTCT ACTTTAACTA 100  
AATGTAAGGA AGAAAATATA CAAGCCCATA TTTAATGTAT TTCTATNCGA 150  
GCAACAATAG TTCATATGTT CATGTTTGCT ACTATCACAA TTCAACATAT 200  
GAACACAGAT CAGCTCTATA CCATGAATAC TGCTGGAAGT GATGGTTTAG 250  
GATTA 255

20

## (2) INFORMATION FOR SEQ ID :512:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :512:

GAAAGATTGG ACATGATTGC GTTTATAAGA ATGAGAGTGT TAAATTGGAT 50  
TTCTTGCTTT ATTTGTGACA TTTCAGTTA TTAGAAATCA TGTTACCATT 100  
AGAAAAATTG AAGTTTCCTA GTAACAAAGT AATTGATTT GTGTAACCTG 150  
ATAAAAGATT TACTGACTTA AGCTTTTGTT TTTTTCATA AGCTGCTTTT 200

40

268

GAGCTTTGTC

210

## (2) INFORMATION FOR SEQ ID :513:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 222 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :513:

15 CTGTACAATC ATCCTGCAGA AAATTGTTTT GGAGAATTCT TGGTAATTGA 50  
AGACCAGCAG AGCAGCCCTC CCCACCCGCC CCGTAAAAGT GCTTACAATG 100  
AACAGGGATT CTTTCTTTA CAAAAGACCC AAAGATACGT GGACAAAAAA 150  
20 AGAAAAGCTT GAAGTCTCAA TGCCTAATGT GTGCACATAA AACAGGCACG 200  
AAGAAACAAA CGTGTGCATC CT 222

## 25 (2) INFORMATION FOR SEQ ID :514:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 240 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :514:

GCAGGAGAAG GAAAAGACAG CAACTCATCC CAGAATTGCC NAATGAAGAT 50  
GAGGAGAATC CCCTCAAAGG GATCTGTGTG CTTACAGTGG TGACAGTGAC 100  
40 AATGAGGAGG ACTGATGAGA GACTCAAGAG TGAGGAAGAG AGCTAGCTGA 150

269

CTGNAAGAAA TGACCTGTCT NNTCTNCAGC GCCATTCCCN AACAGATGCC 200

CTAGTCAGGA CCACAACTCT TAAACCTCAT AGCNAAATAT 240

5 (2) INFORMATION FOR SEQ ID :515:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :515:

CAATGCCCAA TCTGAGTGTA TACACATCTT AGGAAAAATA ATCTAANGTA 50

ACTTTTGAGG GTGAGAGNGG AAATAAGAGA TCACATTAT TCAAGACTGA 100

20 TCCCTATNAG GAAGGAGAGG CCCAGGCACA GATACCACAA AAGAGCACAG 150

TACCCAGCTG TCCTGGNATT GNTTGAGTGT AAG 183

25 (2) INFORMATION FOR SEQ ID :516:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :516:

TCGCAGCAGA AGGAAGTCGT TGACCTGGCA GCCAAGGGAA CACACAAACA 50

CACTCACACA CACATGCACT CACCTGCATA CACACACACT CATACACACG 100

40 AACACTCATA CACACANGCT TGTGCACACA TGTTCATGCA CATGCATGCA 150

270

CTCACACTCA TACAAACGCA CATTTAAACA CGTGTGNACA NTGTACTCAG 200

ACACACACAG GTGTG 215

5 (2) INFORMATION FOR SEQ ID :517:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :517:

TCGCAGAGAA GGAACAATCA GGGCCATGAC AGGAACCGCA AAGAACCAGA 50

GGGTATAGGC AGCAAAGAAG GGCACATAAA AAGGCTGCTT CTCAGGAAAG 100

20 TGTCGCAGTG AGACAAACAC ACATACAGAC CACACACAGA CCACCACCTC 150

AATCATGGGC CCTAGCCGNC CTNGTAATAC G 181

25 (2) INFORMATION FOR SEQ ID :518:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :518:

ATGTAACTCA ATCCATCCGC AAGAAAACCA AACCAACAGA AAAGGAAGCT 50

GAAGACATGG ACATCGCAAG CCACGCGGTA ATGCATACTT GGCACAGAGT 100

40 AGCCAATATA GAAGACGTGT GCCTCACACG GTTCACTTTG TTCATCAATA 150

271

AAAGAATATA AAAATCTCGT TCACCCAGTG GTAAGTGTAT TAAAATAGAT 200  
CTGTATCATA CACACAGTTT CTCCCGGAGT CGTGAGAATG ACAGGAGGGA 250  
5 CCTGGCAACT 260

## (2) INFORMATION FOR SEQ ID :519:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 115 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :519:

AAGCTAATAC AATGGTCATT TCCAGACAAA TTAAAGGAA AACTAAGGC 50  
20 TGCTTCAAAG ATTATCTGAT TCCTTTAAAA TATATGTCTA TATACACAGA 100  
CATGCTCTTT TTTA 115

## 25 (2) INFORMATION FOR SEQ ID :520:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :520:

CANGTGGCTT CAATTAAACA ATNAGGAGCC TCNNAACATC CTGTCGCAGA 50  
AACTCCCAAT ATAAACGCCC CCANACACTA ACACAAAACA GCCTTATTAA 100  
40 CCAGATAAGT TCTCCACTAC CACTCCTAGA TTTGATGTAA CCCTGAATNT 150

272

GACTNATAGN TNGACCCACC TGTGA

175

(2) INFORMATION FOR SEQ ID :521:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 136 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :521:

15 ATGGAATCAA ACAGCTCTAT AATGAAGATA ATGTCTCAGA AAATGTGGGT 50  
TCTGTGTGTG GCACTGATTT ATCAAGACAA GAGGGACATG CTCCCCCTTG 100  
TCCACCTTTG CAGCCTGTTT CTGTCATGTA GTTCA 136

20

(2) INFORMATION FOR SEQ ID :522:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 200 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :522:

AATGGAGCAA TTCATCCAGT TCTTCTAGAA ACAGCTCAGA ATCAAAGCTG 50  
35 GATATATTTT GTGTCTTCTG TGA CTGTTCA TTCATGGAAG GAAGCAGACT 100  
GCTTTGGGCA GAATTATTCT CCTGACTACT TGAGCTAGTA GACTAGGAAC 150  
TATTCCATAA GAGGAAATCC TGTAAGTCTT AAATCCCCAC TGGAGAAAGC 200

40

(2) INFORMATION FOR SEQ ID :523:

273

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :523:

10

AGTAAGGTTT TGCATCCTTT GATCAGCAGG TAACTGACGA ATTCTTGAGT 50  
CGAAGATTAT ACCTTGATGA GCTTTGATGA GCTCTTGCAA ACGAATGAGA 100  
CCAGTGCTGT CATCATACAC AACCATGACG TTTTCCACTT GAAAACTGC 150  
ACCAGGTCTA AAATGCACGC TGAGTGAAGA GAACTCTGGG CAGAGACTGA 200  
CATA 204

20

## (2) INFORMATION FOR SEQ ID :524:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :524:

ATATCTGTCT CATCATCCCA AGGTTTCACA TCTAGTAAGA TGGAAGACTT 50  
GGCAACAAGT GCAGGTTTTT TGGCTTTCCT TGATTCATAT TGTGCAAGAC 100  
GTTCTTCCCT CAGCCTCTTT GCTTCTTCAC TTNNTCTAAN ATAATCCAAA 150  
GAGGTCAATG TATCATCA 168

40

## (2) INFORMATION FOR SEQ ID :525:

274

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :525:

10

AAACTGTTCT TTAAAAGGCC TCTCCTGGTT ATTAAGCCAG GAAGAGAAGT 50  
AGAATCTCGA ATCACCTAAN GGAAATGGTG ACACAGGTTG TCCTTTCTCA 100  
GCCGTTGGTT TCCTTTCATC TCTGAAGGCC TGTAGTACCA TGAGGAAAAC 150  
ATTTAATTTA GAGGGTGAAC CCAACAGTAG GAAGCTGAAA GCAGAAGTGT 200  
TTATCTCCCT CTGCATTAG ACCAGGCTCC TTAGTGCACT CATCAGACTA 250  
TCGCTGCCCC TGCTGTCTGC TGTTGAGCCT TCACCACCAC T 291

20

## (2) INFORMATION FOR SEQ ID :526:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 207 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :526:

CATCCGCGTG CTGGACCCCT TCACCATCAA GCCCCTGGAC AGAAAAC TCA 50  
TTCTCGACAG CGCTCGTGCC ACCAAGGGCA GGATCCTCAC CGTGGAGGAC 100  
CATTATTATG AAGATGGCAT TGGTGAGGCT GTGTCCNNNN GTAGTGGGCG 150  
AGCCTGGCAT CACTGTCACC CACCTGGCAG TTAACCGGGT ACCAAGAAGT 200

40



275

GGGAAGC

207

## (2) INFORMATION FOR SEQ ID :527:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 218 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :527:

15 AGCATTCGGT AAGGACGGAC GTGTTCAAGG ACAACTTTGA TGAGATGGAC 50  
AGGTCTAGGG AGGTTGTTCA GGAGCTCATT GATGAGTACC ATGCGGCCAC 100  
CCAGCCAGAC TACATTTCCCT GGGGCACCCA GGAGCAGTGA TTTCCCTCCC 150  
20 CACTACTTCT TTNCTTAGAT GGTAACCACA GCCTCGACCA TGCCTGCTCC 200  
CTCTGACCCA GCTTCACC 218

## 25 (2) INFORMATION FOR SEQ ID :528:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 229 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :528:

AACCTNATGA CTCTCCATCC CTTGAACCA AACATCTAGC ACTCAGCTCC 50  
AGCATATTTC ACCATTCAAC CCGAAATTCA CAAACGCTAC TTGTCGACTT 100  
40 GTAACCAATT TACTCAGCAA GTGCTGACTC CTTAACGGAT CATCCCCATC 150

276

CTNCGCTGCA AGGTGACTCA CTAAATCAT NTGTTAACAC CAACATTATT 200  
TTTACACCCA GTGTGTAAGC CAGAAGGGC 229

5 (2) INFORMATION FOR SEQ ID :529:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :529:

ATATTATTCA TCATCCCAAG GTCACATCTA GTAAGATGGA AGACTTGGA 50  
ACAAGTGCAG GTTTTTGCTT TCTTTGATTC ATATCGTGCA AGACTTCTTC 100  
20 CTTAGCCTCT TTGCTTC 117

(2) INFORMATION FOR SEQ ID :530:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :530:

35 TCGCAGCAGA AGGAAGCTGA TCCACCATCC GGACAACCCG AACCCAAGCT 50  
GAAGACGAGA AATGATCCAG AAAGAATGTG CTGCAATCCG GTCATCTTTT 100  
AGAGAAGAAG ACAATACACA CCAATGTCGA AATGTGGCAA AATTACTGTA 150  
40 TATGCACATG CTGGTGCTAC CCTCTCACT 179

277

## (2) INFORMATION FOR SEQ ID :531:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :531:

AAAGCATTCA AGTAAGAATA TGGCAATAAA AAACAAAAT ATCTTCTCAG 50  
CATTCAAAC AAAACGCATA AGTCATTCCT AACTNAGAG CTTTATAGCA 100  
TTTTCCTAGA CAGGAAGGGA AAAACAGTT AGCATTTAAA AGTCCGAAA 150  
GCTTTTTCGT TGNNTTAATT ACATCAACNN TCTGCCTTG TCCAAATCCC 200  
TTAT 204

## (2) INFORMATION FOR SEQ ID :532:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :532:

AAAGGAGCTC AGAACTTCAG CTTGAGCAGG AAGAGGAGGA CGTGCCAGAC 50  
CAGGAACAGA GCAGCAGCAT CGAGACCCCA TCAGAGGAGG CGGCCTCTCC 100  
CCACAGCTGA GGGGCTGGGC TAGGGGTGGG TGGAGCCCTT TTAAATACC 150  
CTTCTTCAA AACTTAGCTC TGAATGGAGA AAC 183

278

## (2) INFORMATION FOR SEQ ID :533:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 287 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :533:

GAAACAAGTT CTCGCTCATC CCTGCATTTC TGCCAACTTC AGCTTGCAAT 50  
ATTTATACTC CAGACTATTT TCATCAGACA AAAACCAGTA AGCAGGGTCC 100  
TCTTTGAGAA GAGTTCTCTC TTTGGGAGAC AGGCTGCCTT CGATGACACG 150  
TTTCACAAGC TGGTTGATGG TGCCCACTAC CCGTGATCTG CTCGCTGGGG 200  
GACAGCATCA CTCAGACTAC TTGGAGCCTT GCCTGAATTT CAGGTTTCGT 250  
AGGAGGAATA ATTTTCTCCT TCTNTNGTAT CGNCTCT 287

## (2) INFORMATION FOR SEQ ID :534:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :534:

AGCCACTGCC CCTCTTGTCT ACGTATTCCC AAAATTAAAC TTTGATGCCT 50  
GACTTTTTGC AGTCAGTTT AAGTGAGCTC CCTGAGGTGC CAAGGCCATG 100  
GTGTCCCCCT GCTGCGTCTG TTCGTCAGCT GAGTTCTTGT GAATCTNTGT 150

279

TTAG

154

## (2) INFORMATION FOR SEQ ID :535:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 212 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :535:

15 GATTACCCTA TATCTACAAT TNGAGGTAAA ATAGAAGCAA CACATAAAAG 50  
GGCCTATTTC TGCTACCATG TCATATAATT CTCCATAGTG AATATTGTGA 100  
TAAAGCTACT GAAAACTATG CCTCACAGAG CCTAGCTTCT TGTAGAGCTG 150  
20 GTATTTTACA ACTCGCATTG CTTGGAAATC TCAACACACG TAAGACTCTC 200  
CTAGGAAGGC AC 212

## 25 (2) INFORMATION FOR SEQ ID :536:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :536:

GGAAGCTCAA TGTCCGGCAG GTCAATGCTT CNCGGACACG GATCATTTTT 50  
ATCTGATTCC AGCCTGCTTG CAACCCTGGA ATCCTCTTGT TCCCTGCTGC 100  
40 CTGCCCCTTG GGAAGGNA CA GTGATGTCTT TAGGGGAAGG AGGAGCCCCT 150

280

NTCGGCAGTT GTCTTACT

168

## (2) INFORMATION FOR SEQ ID :537:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 147 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
10 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :537:

15 CGGATCATTT TTATCTGATT CCAGCCTGCT TGCAACCCTG GAATCCTCTT 50  
GTTCCCTGCT GCCTGCCCCCT TGGGAAGGNA CAGTGATGTC TTTAGGGGAA 100  
GGAGGAGCCC CTNTCGGCAG TTGTCTTACT AGGNNNTAA TGAAGTA 147

## (2) INFORMATION FOR SEQ ID :538:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 250 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :538:

30 GTGGAATCTC AATAATGACA CAAGGTACCA ACTGCCAGCA TTTCTGCGAG 50  
35 GCAATCCTGC TCTTAATCTG CAAGATGGAC CCTTCTGCAG AGAGATTGCT 100  
GTGGGTGATT CTAAGGACAG ATTGTTATAT ACGATGTGGG AGAGCAGATT 150  
GCTGTTCCCC GCAATGATGA ATGGGCACGG TTTGGCCGAA CACTTGCAGA 200  
40 AATNAATGTA AACCCNAACT GATGTAGAGA GGACGCAGCT GCCCNAATAC 250

281

## (2) INFORMATION FOR SEQ ID :539:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :539:

AGAAGGTAAG GGAGTGGGAG GCAGGTGGGT GTTCTGGAGG GGGTATCCTT 50  
GTGCTCTAAG GGTGCTATGT TCGATGCTGG TGTTCGGGG ATGGTGAATG 100  
CCCTTCTTTA ANNTTAGAGG GAAATCCAAA CCAATAGGCC CCAAGGTTGC 150  
CAGTGGGATA GGGGTGTAAA AAGTAAATT GGGC 184

20

## (2) INFORMATION FOR SEQ ID :540:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :540:

AACTTATAGA AAAGTAAAGG AAACCCCAAC ATGCATGCAC TGCCTTGTGA 50  
CCAGGGAAGT CACCCACGG CTATGGGAAA TTAGCCCGAG GCTTANCTTT 100  
CATCATCATG TCTCCAGGG NGTGCTTGCA AAGAGATATT CCGCCAAGCC 150  
AGAT 154

40

## (2) INFORMATION FOR SEQ ID :541:

282

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :541:

10

AATTGAATTC TTAAGAAGCT GTCAAATATG GCAGTCTTTT GATGTTAGTA 50

ATTTTGT TTTT CTTCTGTGTT ATTGTTCAA AGTACTGGCC TTTTCCTTCA 100

15

TTTCCAGTAA TTATTTTATA ACTATCACTT TTAATTGAGT GGAAATTAGA 150

TGATTTGGTT ATACTGTGAA ACAGC 175

## (2) INFORMATION FOR SEQ ID :542:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :542:

30

AAGTACCTTT TCCTGCAGCT GCCCGTATGC CTGAGTGACT AAGGGGCAGT 50

CGTGAGAGGC AGAGTCCAAG ATCTCATTGG TCGTTTCCAG ACTGCCGTCC 100

35

AGCCGTGCTG CTTTCATCAGG GCACACTCGC CGCCCTCCTG GGGCCAGGTT 150

GCACATGTAC AGGTACCCGT CGGCGCACCC ACCAACAACG CGGTCTTCTG 200

AATCGCGACT GGCNAACAGA T 221

40

## (2) INFORMATION FOR SEQ ID :543:



283

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :543:

10

AAGTAGATAG CTTGCATCCT GACACCGTGG CAAAGTTAAG AAAGTTGAAG 50  
GAGAAACATA CCTTGAGAGG GGGTTTCTT TAAACTAGT GTTAGAAGCT 100  
TAGGGATTTT TTTTTTTATT CCTTACTAAC TTTCACCCAG AACCGCTCTA 150  
TTTGA CTGTG GCCGACATTG CAACTTTNT GACAGG 186

## (2) INFORMATION FOR SEQ ID :544:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :544:

30

AGCATCCTTG CCACCTCCCC ACCCGGGAGT CAAGGGTCGT GGTTCGCCT 50  
TGAACAGGCC ACAGCCGTAG CTGTAGAGAG GCCAGTGGTA CATCAGCCCA 100  
CCGACAGGAG GAGGAGCCCT GGCTTGAGGG AAGGGGAAGC CCAGGCCTGT 150  
GCC 153

## (2) INFORMATION FOR SEQ ID :545:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 161 base pairs

284

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :545:

|    |  |     |
|----|--|-----|
| 10 | GATTCAGCTC CAGCATCCTT GCCACCTCCC CACCCGGGAG TCAAGGGTCG | 50  |
|    | TGGTTCTGCC TTGAACAGGC CACAGCCGTA GCTGTAGAGA GGCCAGTGGT | 100 |
|    | ACATCAGCCC ACCGACAGGA GGAGGAGCCC TGGCTTGAGG GAAGGGGAAG | 150 |
| 15 | CCCAGGCCTG T   | 161 |

## (2) INFORMATION FOR SEQ ID :546:

## (i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 20 | (A) LENGTH: 188 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :546:

|    |  |     |
|----|--|-----|
| 30 | AATAGCCCTG AGGTCATCCT GCAAAGTGCG TATCAAAAAA TACGAAGTTA | 50  |
|    | GGGTGACAAA GTTTGACAGT GATGTTATAC AAGTCAAAC TGAAGGTCA   | 100 |
|    | TAGTAAGCAT ACCTATGCTG AGAGAAAGCA TCAAATCCTT TGTGTACACA | 150 |
| 35 | TTTAGTTTTA TTGTAACAAA GCAACTTGTA CACTTTTA              | 188 |

## (2) INFORMATION FOR SEQ ID :547:

## (i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 40 | (A) LENGTH: 218 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |

285

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :547:

ATNCCTTCTC CATCCANTTA GTTANCAGAA ACTAATCAAA AGAAAGTCTG 50  
ACAACTGCAC TCCCCCTTGC ATGCCATTCT CTCAAGCCCA TAATCTTGGA 100  
GTATCCACAA CGTGCGAAGG CCTACCCTTT GTGTGTACTC ATCTCACGTT 150  
TACGTATTTT GTNGTTGAGG AGCTCCTCTA CAAATGTTGC GTATCTTCCG 200  
AATCACTCAT TTAGAAAA 218

(2) INFORMATION FOR SEQ ID :548:

(i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 46 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :548:

GGAGGAGACC ATCAGNCCCG TGAAGACCAC TCCTGACGTC TCGTGT 46

30

(2) INFORMATION FOR SEQ ID :549:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 146 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :549:

286

AGGGGGCTAA NGGTTGGGGG CAGGAGGCAT TGCTGATGAT CTTGAGGCTG 50  
TTGTCATACT TTTCACGGTT CACACCCACG ACGACACGGG GACTCAGCAG 100  
5 AGGGGCAAGA CACGACCTTT AGTTTCCCCC TTGCGATAAN CTTNC 146

## (2) INFORMATION FOR SEQ ID :550:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :550:

AAATATNGAN TATCCATCCC CTCAGCATT TATCCTTGT GTTACAAACA 50  
20 ATCCAATTAT ACTCTTTCAG TTATTTTAAC ATGTACAATT AAATTATTAT 100  
TGACTCTAGT CACCTTGTG TCGAGCAAG TACTAGGTCT TATTCATTCT 150  
25 TTCTAACTAT TCCAGGCCCT TTTTAATCAA GAAGGCTCCC TAGACCAAAA 200  
TTTTAAAAAG ACAATGCTAG G 221

## (2) INFORMATION FOR SEQ ID :551:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :551:

40 AAACATCGTT TATTCATCCA GCAGTGTTC TCAGCTCCTA CCTCTGTGCC 50

287

AGGGCAGCAT TTTCATATCC AAGATCAATT CCCTCTCTCA GCACAGCCTG 100

GGGAGGGGGT CATTGT 116

5 (2) INFORMATION FOR SEQ ID :552:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 150 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :552:

CTCATCCTCT CCTATTACAT AGTGAAGCCC ATGNCAAATA GGAAGAAGCT 50

CAGTATCGCT CCTCCCACCA TAACCCCCCT TAATGCCTCC TGAACCATAG 100

20 TTNCCTCCAC TATATATCCC CCCATGTTCC TGCTACCCCA AGTTTTCCT 150

(2) INFORMATION FOR SEQ ID :553:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :553:

35 ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT 50

GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTTGCATGAC TCTACTATGG 100

GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG 150

40 NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATAT 189

288

## (2) INFORMATION FOR SEQ ID :554:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :554:

ACTTATTGAA ATAGCAGACA TTTCGCTAGA CACTCCAATT AACCTGATAT 50  
15 GAGGCGCTAA TCAATAAAAA AAGTTAAACA TTTGCATGAC TCTACTATGG 100  
GAATAAATTA CCTGTTTAAT ACCTCGACTT TTTATAGAAA AATAATGATG 150  
NCCAAGGTAA ACCAGGTAAC CCAGGCCTGT GAACTATATG CCTGGAAC 198

20

## (2) INFORMATION FOR SEQ ID :555:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 97 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :555:

CAAGCTGAGG AGCAAGGAGA GCCAGTCTGA GTCCCAAAC TGAAGAACTT 50  
35 GAGTCTGATG TTCGAGGGCA GGAAGCACCC AGCACAGGAG AAAGATG 97

## (2) INFORMATION FOR SEQ ID :556:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 269 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

289

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :556:

TCTGCTGTCT GTCGCAGGAG AAGGAATGTC AGAACTTCA TCCTCTTGTT 50  
GGGGAATGCA CCCTCNTGAG TAGGCTGACC CATGAGGCTG TGGGAATTGA 100  
10 GTCTTAGGAC ACAGAGACCA GGGTGTGAA TTTTCTTCCC TGCCCCTAGG 150  
CTGTTCAAGGT CTCCTGCAG CAGTCAGGGC TGCAAGCCCT GGAAAGGCAT 200  
15 CAAAAGAGGC CCAGCTCCAG GATCGTGTGT ATGCTCTCCA GCAGACAGCT 250  
CTTCAAGGGT GATCTTGTT 269

20 (2) INFORMATION FOR SEQ ID :557:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 245 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :557:

ACTCCCTCAA GGTGCTGCGT CTAAGCCTAC AAGAAAGTTT GCCTATCTGG 50  
ACCCTGNCTC ACGAGGTTGG CTGGAAGTAC CAGGCAGTGA CAGCCACCCT 100  
35 GGAGGAGAAG AGGAAAGAGA AAGCCAAGAT CCACTACCGG AAGAAGAAAC 150  
AGCTCATGAG GCTACGAAAC AGGCCGAGAA GAACGTGGAG AAGAAAATTG 200  
ACAAATACAA AGGTTCTCAA GACCCACNNA CTCCTAGNTT NAGCC 245

40 (2) INFORMATION FOR SEQ ID :558:

290

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :558:

10

GAATTTAAAA AAAAAGAAAG AAAGAAAGAA AGGTTCCATC TTAGATTCTC 50

ACAACCTTCG TTCCGCAGTT CATTAATCCG ACTCTGATGC TAAGGTGACA 100

15

GTGTATGTAA GTAGATTTTT GTTTTCAGTG AAGGAGACCT GGGAAAAGAT 150

GGATTTCTCT CTGTATCTTA AGAGTTATCA GAT 183

## (2) INFORMATION FOR SEQ ID :559:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :559:

30

GTCATCTTTG GAAAGTGAGA TAACCAAGGA AATAATCGAA GGAGTTAGGG 50

AGATGATTAC GTGATAATGA CTTTGGGCGC TTAACCTTTG ATCCCGGGTA 100

35

TGCTNAAGAA GCTGAC 116

## (2) INFORMATION FOR SEQ ID :560:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double



291

(D) TOPOLOGY: lin ar

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :560:

CCTTGATGAT ACCATTATCC TCATTATAGA TGATGCACGG GCCCCTGCGC 50  
TGGATACGGC GACGGTTTCT CATTTGCCTT TGTCAGCTCT CATTGCTGA 100  
10 GAGGCATAGA CCTTTTGTGAT ATCATCAGGC TTTCGGTTT TAGGAGCAA 150  
ACAGCTTCTT 160

15 (2) INFORMATION FOR SEQ ID :561:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :561:

GCAGTTGGCA GGTGCACTAT CCCAGATGGG CCACTAATAG AAAGTTCCGC 50  
AAATGCACCC CGTTCCCCTG TGCGAGATCG TTTGAATNAG ACCAGAACT 100  
30 G 101

(2) INFORMATION FOR SEQ ID :562:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

292

## (xi) SEQUENCE DESCRIPTION: SEQ ID :562:

ATAAGTTATA GCAAATACAG TCTTCACAGA TTTGAGTAAC TTTATTCGAT 50  
5 TTTATAGTGA TTTCTTAAGG CCTATATCCA ATGAAACCAT TTCCAAGCTC 100  
TATGAGGAGT GGAATTTTAG ATGTCTATTA CATNGTCTT TTAAAAGAAA 150  
AATGCTTAAC NNCTAGAATG AGCAAGATTA CTT 183

10

## (2) INFORMATION FOR SEQ ID :563:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :563:

AGAGACACGT GAAATTCATA TCTCAAANNC ACAGAGCTGA GACTTTGGGC 50  
25 CTAAATACTG TACCACTGGT TCCCTGAACC AAGGAAGAAA AGTGTCGGTA 100  
AAGGCCCGTT AAGACAAGAT GGCAAGGAAA AGCACCTTAA ACAATGGTAA 150  
GATTTATGTT AGATCAGTGG TAAGAGTTTC TAGTGAC 187

30

## (2) INFORMATION FOR SEQ ID :564:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :564:

293

GGGACCCCAA ATCACATCCA GAATACTAGA GTGAGGCAGC TGCAACATGA 50  
 CACAGAAAAA TGAATCAGG ATTTAGGGGA ATTGGATTTC AGTGCCTATT 100  
 5 GAGACACGAT CTAGGAAGCC TACCACTTTG GCTGCTCACT GTATGCACAC 150  
 AACCCNANNA NAATNGATGA AAACAAGAAT GTACAGCATG CTCCTAACAC 200  
 AANGTGAATA TTC 213

10

(2) INFORMATION FOR SEQ ID :565:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 167 base pairs  
 15 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :565:

TCCATCTGAC ATCGCATTTC CATAGAAATG GCCAAAGAAA GAAGGTCCTG 50  
 25 GGGTTTTTCA TAGAAAGCTC AAAAAGTTCA ACCTTGATGC TATCCCCCAG 100  
 CCCAATACAA AATACACAGA AAAAGCAATT ATTAAAATAC TGGCTTCGGT 150  
 TTCTTTTTTT CCTTTAA 167

30

(2) INFORMATION FOR SEQ ID :566:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 128 base pairs  
 35 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :566:

294

GAAGATACAG AACCATCCGT GAAAATCATT TAGCACTGGA GACCTTCTTT 50  
GTATTACTTC CTNGTTACTA GACCTCTAA TTCAATGGGG CCCTGCTGGT 100  
5 TTGTCGATGA ATTGAGCAAC TGAGAACG 128

## (2) INFORMATION FOR SEQ ID :567:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 202 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :567:

GGAGGCTCGG GAGTAGCATC CTCAGGAGTA GTGTAGCGAG CAAATTTGGA 50  
20 AAGTAGTCCT CAATCTTCGA TTTCCAGCA AGGACTTTCT CAGCNAGCGA 100  
TCTCGNTTGT TGAGGAACGG ATCAAGAGAT GNNNGTNTAG CTGTNNTGTT 150  
25 GTTTAGATGT CTTGAAGAGG TTAGAGCCTC CTGTAGGCGG TTGGNNTGGG 200  
NG 202

## (2) INFORMATION FOR SEQ ID :568:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :568:

ATGTCATGAT GCCTAACTCA TACACTCTTT GCCTCAAATA TAATTACTAA 50

295

AAACAAATAT AGTATAAACA TTAAACAAAT GAACAATAAT CATCAATAGA 100  
CGGGTTACTT TCAAGGAAGA GTTGTTTGT GACAAATTCT ACTCTTGATC 150  
5 TA 152

## (2) INFORMATION FOR SEQ ID :569:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :569:

CAGGTCCGCG TGCTCTCCGC ACCACCCAC TTCATTCCGG CCAAACCAAC 50  
20 CGCACCCCTG AATTTCTCCG CAAATTCCT GCCGGCAAGG TCCCAGCATT 100  
TGAGGGGATG ATGGATTCTG TGTGTTTGAG AGCAACGCCA TTGCCTATTA 150  
25 CGCGAGCAAT GAGGAGCTGC GGGGAAGTAC T 181

## (2) INFORMATION FOR SEQ ID :570:

(i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 157 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :570:

ATCCCTTGGG AGTTTATTCT CCTGGTAAGC TGTAATTGCA TATCCAGTTT 50  
40 AACTGGACTG GGCTGTGTTG GGCGAGGATC NGCAGGGTTT TTTCCNNT 100

296

NGAAAGATGA AATAGATTNT TGAGCACTGG NTGCAGAGCC AAAATGCNTA 150

ATGCTTT 157

5 (2) INFORMATION FOR SEQ ID :571:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :571:

GGCACTAAAG CCTTTAATAA TACGAGATGA AATGCAACNG TGNNATGACA 50

AGTAAGTGAG CCTGACCTGG CATTGCCTCG CCTCACCGCT GGCTTTGACC 100

20 AGGGTATGAT CTTTAACTTT TCTGAGCTGA TTTGATCGTG GTCTTTACAC 150

ACAGGTGGTC GTTCCTGTTT GGACACTGTT TTATTTGTTT GAC 193

25 (2) INFORMATION FOR SEQ ID :572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 179 base pairs

(B) TYPE: nucleic acid

30 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :572:

TCGCAGGAGA AAGAGGTTTT CAGAGGCCCT GAGGACATGG CTGCCCTTGA 50

GAAGGATTTG AGGAGGTTGG TGGAATTTGT TGAAGGAGAG GGCGAGGAAG 100

40 AAGGAGAGGA TACTAAAGTT AAAACGTCAC AAGGTGTGCT TTTAAGGGAG 150

297

CTTTCCTGTT TTAAACATGA AAGTGTGGC

179

(2) INFORMATION FOR SEQ ID :573:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :573:

15 AGGACCTCTA AGACATCCTT ATGACGACAG TTTGTCCAA GGGGATATCC 50  
ACAGAGTACC TTGTGGCATT AGGTGATTGT AGTCATACAC TTAAAAAGA 100  
TTTTATTTCT GATCTTTTGG CGATCTTCTT CTGCCCATG NNGCTGTAC 150  
20 TTNGCNCGGG NAGCGGTAA TTCTANCCGC TAGGTGTGC 189

(2) INFORMATION FOR SEQ ID :574:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 262 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :574:

35 GTGCCTTCTA GGTTTTGAAC TTCTATGCAT TAGCGCAGAT GTGGAATGCG 50  
TAAAGGTGTT CATAGTTTGA CTGTTTCTAT GATGTTTTTT CAAAGAATCG 100  
TCCTTTTTTG AACTATAATN CCCNCGGTT ATTTTACCAT CACAGTTTAA 150  
40 ATGTATATCT TTTACGTCTC TACTCAGACC ATATTNAAA GGGGCGCCTC 200

298

ATTATGGGGC AGAGAACCTT TTAATAAGTC TCATTAAGAT CTGAATTTTG 250

GTTCTAAGCA TT 262

5 (2) INFORMATION FOR SEQ ID :575:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 56 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :575:

CCAAGGAACC ATCTGCGCCG CAAGCCAGAC CCCACAAGAC CTAGNTTGGT 50

CCTGAC 56

20

(2) INFORMATION FOR SEQ ID :576:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 158 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :576:

GCGAGTCTCA AAGAGTAGAG GAGCGTCTAC TATCTTTCAA CTCCGATCTT 50

35 CTGATGNCGG ACTTTACCGT GACAGCGAAG TGGTATTGTA CGTCCAGGCC 100

CGCCAGCCAC TGTCTTCATG CAGGAACCAC AGTGCCAGAT CCCCACAGCT 150

CGTATCTT 158

40

(2) INFORMATION FOR SEQ ID :577:



299

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :577:

10

GGACCTTGAC CCACATCCAT GTTGAAGAAT GTCCTCTTGT CAAGGTCAGG 50  
GAACAGCACC CACAGAGGGC CTCTGGGTCC CTCTCTGCTC AACTCCCTCT 100  
CTCTCGGTTC CTGCGAGGCT CATAGGGTGC AGGGCCCAGC AGAAGGACTG 150  
AGTCTTCCTC CTGGACTTCT GGTCTGGTA GGCTGTGCTT CATGCTCTCC 200  
TGTCACCTGT ACTGTAAGGA ACTATTATGA CAAACGCATA AAGAATATGA 250  
CTTTG 255

20

## (2) INFORMATION FOR SEQ ID :578:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :578:

35

GAGGAGTCCA TGCCATCCTT GATGAAAAG AACTGAAGA GAAAAGACAG 50  
CCTGTGGAAG AAGCTCAAAG GTTCTTTGAA GAAGAAGAGA GAAAATATGA 100  
CATGATATCT TTGCTTTTGA GTTCCTCACG CTCTCTGAAT TTATTAGTTG 150  
GACAATTCCA TATGCAGCAT TCTGCTTCAA TATANCTCTT NNGGTCTCTC 200

40

300

TCTCTNNAAT ATTTGCCTGT AGGTAAAAGC AAGCTCTGCA TATCTGTACC 250  
TCTTGAGATA GTTTTGT TTT 270

5 (2) INFORMATION FOR SEQ ID :579:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :579:

GAGTTTTCTAG AGGCCCGTGA GGACATGGCT GCCCTTGAGA AGGATTATGA 50  
GGAGGTTGGG TGGATCTGTT GAAGGAGAGG GNAGAAGAGG AGAGGAATGC 100  
20 TAAAGTTAAA ACGTAATAAA GATGCTGCTC TTACGGAAG 139

(2) INFORMATION FOR SEQ ID :580:

25 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :580:

35 GGCAGGAATA CATATAGTCA TCATTGCCAG ACTTAATATG AGAGGTGAAA 50  
TGTTGATCC AATTTATTTT TTGGATAAGT TTTTCTTTCC TATNCCTNTN 100  
GTTTTGATAA TATAATAAAG AAGATGAGGG GCCCA A TATAGAGCTC 150  
40 CTGAGNGAGT TTTNGGAG 168

301

## (2) INFORMATION FOR SEQ ID :581:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 242 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :581:

CGGAGGGCCC TGTTCGGGAA AAATAGGATT TTAAAAATAT GGTTCATTAA 50  
TTTAGGTTTT CTAACATCTA CTTGGGGATG TAGCCTCCAG TGAGGTCAGT 100  
TAAGTGGGAC AGAAACGGCA GAGGGAAGAG GTCTTTGCTT CCCCTGGGCC 150  
CATTCTCCCT GGCTGCCAGC CCTGAAGTC AGAACACCAT GGGAAAATTC 200  
AGGAGTCGGC ACTGTAGCCG TCAAGTGGCG CTACTTTCCA CA 242

## (2) INFORMATION FOR SEQ ID :582:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :582:

GCATTTTTCT TGTGTGCTGT TTATAATAGC AAAGCAG 37

## (2) INFORMATION FOR SEQ ID :583:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

40

302

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :583:

GGAACAAAGA AAATGTACAG AGTTATATGC GCTTTTTTTT GGTATGGGGG 50  
ACAAGAAACA CTTACCAACA AAAATATTTC AACAAACCCA AAATAACTTA 100  
10 CTCACAAATA TGCAAAATTA TCTATGGCAT AGTATTTCGC ACTCGATGAC 150  
ATTTAGAGAT AAAAAATCAA ATGGAGCTT 179

15 (2) INFORMATION FOR SEQ ID :584:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 186 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :584:

AACTGCCATG AAGTAACCTG AAGGAGGCGC TGACTGGAGG GATTGATTAC 50  
AGGATCGGAA CACTCCACAC TCGCATTCT CTGCATATAC CGGTTAGCGA 100  
30 GGCGAGCCTG GCGCTCTTCT TCGCGCTGAG CTAAAGCTAC ACACAATGCT 150  
TTGCGACCAC AATNCACCCT TCATTTCGTA ACTGCT 186

35 (2) INFORMATION FOR SEQ ID :585:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 180 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :585:

5 ACCCACGGTA CTTACATCCT ATGATATGGC CTGCAAAC TA AACTACAAAC 50  
GCACTCACAT CGCTATAATC CTTTAAAGGA CTAAACTTT ACTCCATTAA 100  
GACTTTTATG ACTTCTAACA ACCTCGCCAA CCTCCTCACC CCCC ACTATA 150  
10 CCTCGGAGAA CTTTCGCGTA ATAACCACGT 180

## (2) INFORMATION FOR SEQ ID :586:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 183 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :586:

ACCGACATCA CGANNGACTT GGTCTTAGTT GAGCAATTTG GCTAANNNNN 50  
25 NTNCTNNTTA GCACGTTCTG AGTCTGTGGG ATAGCTGCCA TGAAGTAACC 100  
TGAAGGAGGT GCTGGCTGGT AGGGGTTGAT TACAGGGTTG GGAACACTCG 150  
30 AGANTGGCAT CCTGCATATA CTGGTTAGTG AGG 183

## (2) INFORMATION FOR SEQ ID :587:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 280 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :587:

304

AGGTCAAGTC TACAGCTGGA GACACCCACT TGGGNGNANG AAGATTTTGN 50  
ACAACCGAAT NGTCAACCAT TTTAATTGCT GAGTTTAAGC GCACNTTAAA 100  
5 GAAGGACATC AGNGAGAACA AGAGAGCTGT AAGACGCCTC CNTACTGCTT 150  
GTGAACGTGC TAAGCGTACC CTCTCTTCCA GCACCCAGGN CAGTATTNAG 200  
NTCGNTCTNT CTATGAAGGA ATCGACTCTN TACTCCATAC CNNNCCGATT 250  
10 GAGACTGATG TGACNTTCCT GGGACTGNCA 280

(2) INFORMATION FOR SEQ ID :588:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 371 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :588:

25 GGTGAAGAAA CTCCAGATAT CAAGGAATTG GGAAATCCTG GGCCAAACCA 50  
CCCCAAGATG ATTACACTGA AATGTAGTAT TAGTACTNCT GCCAGATCTC 100  
TTTTTAACAT CATGTGCGTC TCTTGGGATC CAGCAAAAGT GTTAAGCCAC 150  
30 AATGCCCTTG TGCCTTTTAA TATACCACAG TGCCAGTTAA ACTAATATTT 200  
TNTTTTGTG CTTTTTGGGG TATTTTCATT AGTATTTTCTAG CAAATCTCAT 250  
35 GATAAAGGNC AAGGNCAAGA ACTNCAGAGN ACTGAGCAGA GAGGCTNGTG 300  
ATGAAANGTG AAGGCTTCNA CTGACTTTAN GCAGTGGCAG TCANGNTACT 350  
GNGNNGCANG CTTANCTATG A 371

40

(2) INFORMATION FOR SEQ ID :589:

305

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :589:

10

GAGAGAGAAC ACTCCCCTCC ATCCCAGCAC TATGCACAGT TCACGGCTCA 50  
TATGCAAAGT GGAAGACACG TGGGACAAGA GCAAAGCACA AGTGACACAT 100  
GGTCCCCTCTC TAACACCTCA GCACACCAAC CCTGACGCTC CCATCACAGA 150  
TGCTGNTCAT TCTTNCACGG NCCCCTTTTA TAAT 184

15

## (2) INFORMATION FOR SEQ ID :590:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :590:

30

GGGGGCCCCG CGTNCACNCC CCCACACTCT TGGTAGGCAA TGCTTGTCCTC 50  
NATATAGTTG NNGTCCTATC GAGTGACACT CTCGTTTCATG GATANGGTGN 100  
GTAAAACCCN TNGTNGCATC CNNATTGGGN GCANTGNGCC TNTCCCCTTN 150  
AANGGTTTTT GCNTNCACTC GACCTNGGGA GGATTCAATG NACNNNCTNG 200  
CANTGGNCAA GCNTTGNTTG CNNGNATTGA GAACCCNCCA ATT 243

35

40

## (2) INFORMATION FOR SEQ ID :591:

306

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :591:

10

ATTCGCCNN TAAGTAAGTC GTNATTANAC GCGACGNCTA CTA CTGAGAC 50  
NCGCATGCGC TCTCTCTACA CTAAAGCTCG TCGCTNGNTN ACTTGCGNGN 100  
NAAAAAACC CCCTGGGNNC GCTTTTCACC CCCAACTTT CAAATTCCGC 150  
CCCTTTNGGC NANGCCCAAC CANNCCCCC CCCTTTTNC CGNCCCANNC 200  
TTNGGNCNTA ANNATTNAGN CGGNANGNNN GGGCCCCCGG CCAACCC 247

20

## (2) INFORMATION FOR SEQ ID :592:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 425 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :592:

35

GGAGGGGAGT AGAGGAAATT TTCATTCTGG AAAAAATGC ATACTGTTTG 50  
ATATATTACT CNTCATGCTT TCCACAGATA TTATACACAG ATATTATATT 100  
CCANGGATTA CGTTGCAATG TCTTCAAAA TAGANAATTC ATTTTATATT 150  
TCTNGATGAA ATATAATAGT ANCTNNGCTA CTTTGGGAA TGTGACAAAA 200  
TACTATGATG ATTACAAC TC ATTAAAGCAT AAATNTGCAT GATTTA ACTN 250

40



307

CATGTTTCCTT CTATGANCTN CGTGGNATAT AGGCATATTT ATTAATGCTA 300  
TTTANGGCNT NNGTGCTTTG TAATGATTCG NCNTTAGGTG AAGGGNTACT 350  
5 TTTNTNNTNC TTCNTAGTAG ATTNNGNTTN NTCTTTTAA GAGGANTCNA 400  
NTTTCATGNG TAANCATCAT CTTTT 425

## (2) INFORMATION FOR SEQ ID :593:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 258 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :593:

20

CGCTGCATGC GTCAGCGCNA CGCGACGACA GCGCGCGCGA CGCGCGCGAC 50  
GCACAAAANA AATGCATGCC AACACGAANA TATGTGCACA CAAACGCAAA 100  
25 CGCGTGTGAA CACATGCGCG CNNGCGGCNC GCGATNCAAA GCTGAAATGT 150  
GCNNGNCNGT CGTGNGCGNA AATGTGAAAT GAACAAACAA CAATGAATGA 200  
ATGAATGTGA AAAAGAGNGN GNTTGAAAAT TNTANAGNNC CCCCCCNTNA 250  
30 ANCAAAAG 258

## (2) INFORMATION FOR SEQ ID :594:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

308

## (xi) SEQUENCE DESCRIPTION: SEQ ID :594:

|    |  |     |
|----|--|-----|
|    | GACCCTAACA ATATGTACAA AAATATAAAA TGTAATAAAA AAATACAAAC | 50  |
| 5  | AAATTCCTT TTTAAAGTAC TTTTAAGAAA AAAAGCAGGG CCTTGGAAGT  | 100 |
|    | TTTGGTCTT TTTTCCTCCC CTGTTGCAAA TTCTCATGGT TTGGGTGGG   | 150 |
|    | TGGTGGAGAG CGCGTGTCAT CTGCGGGTGC CTGCCCACGT GGGCGGGCGG | 200 |
| 10 | CTCTCTACTC GAAGG                                       | 215 |

## (2) INFORMATION FOR SEQ ID :595:

|    |                               |
|----|-------------------------------|
| 15 | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 272 base pairs    |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |
|    | (D) TOPOLOGY: linear          |
| 20 |                               |

## (xi) SEQUENCE DESCRIPTION: SEQ ID :595:

|    |  |     |
|----|--|-----|
| 25 | GGGGCTGGTT TGGTCATCCG AGATCATTAA AAATGGCTGA CCCTAACAAT | 50  |
|    | ATGTACAAAA ATATAAATG TAAATAAAAA ATACAAACAA ATTCCTTTT   | 100 |
|    | TAAAGTACTT TTAAGAAAAA AAGCAGGGCC TTGGAAGTTT TGGTCTTTT  | 150 |
| 30 | TTCTCCCT GTTGCAAATT CTCATGGTTT GGGTTGGTG GTGGAGAGCG    | 200 |
|    | CGTGTCATCT GCGGTGGCA CTGCCACGGT GGGCGGGCGG GCTCTCTACT  | 250 |
| 35 | CGAAGGTGAC CACGTTTAGA TT                               | 272 |

## (2) INFORMATION FOR SEQ ID :596:

|    |                               |
|----|-------------------------------|
| 40 | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 250 base pairs    |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |

309

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :596:

|    |   |     |
|----|---|-----|
|    | GACAACTGT TGACACCCGG AGGCCTAAAC GAGGATTTC A GCTTCCATTA  | 50  |
|    | TGCCCCAACTC CAGTCCAACA TCATTGAGGC GATTAATGAG CTGCTAGTGG | 100 |
| 10 | AGCTGGAAGG GACAATGGAG AACATTGCAG CCCAGGCTCT GGAGCACATT  | 150 |
|    | CACTCCAATG AGGTGATCAT GACCATTGGC TTCTCCCGAA CAGTAGAGGC  | 200 |
| 15 | CTTCCTCAAA GAGGCTGCCC GAAAGAGGAA ATTCCATGTC ATTGTAGCAG  | 250 |

(2) INFORMATION FOR SEQ ID :597:

(i) SEQUENCE CHARACTERISTICS:

|    |                            |
|----|----------------------------|
| 20 | (A) LENGTH: 225 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :597:

|    |  |     |
|----|--|-----|
|    | CTGCCAAATA CTTTCTTCAC CAACTCATGA GGAGAGGGAA CATGCTGAGA | 50  |
| 30 | AACTGATGAA GCTGCAGAAC CAACGAGGTG GCCGAATCTT CCTTCAGGAT | 100 |
|    | ATCAAGAAAC CAGACTGTGA TGACTGGGAG AGCGGGCTGA ATGCAATGAG | 150 |
| 35 | TGTGCATTAC ATTTGGAAAA GATGTGAATC AGTCACTACT GGAAGTGCAC | 200 |
|    | AAACTGGCCA CTGACAAAAA TGACC                            | 225 |

(2) INFORMATION FOR SEQ ID :598:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 210 base pairs

310

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :598:

|    |   |     |
|----|---|-----|
| 10 | ACAAAACGCA GATATAAAAA AGTTACAAAG ATTTTATAGAT TTTCATTCAC | 50  |
|    | AAAAAAGTC ATTCACATT TACTATATAC ACGTTATGAT ATAATACAGG    | 100 |
|    | AAAGTATTAT GTGCATTGTA AGAGAAGGAA AATAGAACTA CTAGATCACA  | 150 |
| 15 | CGTGTTGTTC TGTGCTCTAA AATACCTAAA GGTGGATTCA TTTAATGCAA  | 200 |
|    | CACCAGGGAC  | 210 |

20

(2) INFORMATION FOR SEQ ID :599:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 116 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :599:

30

|    |  |     |
|----|--|-----|
| 30 | AAAGGAGTTG AGTACTGTAA ACGCAGAGCT ACATAGAAAA AACGGGCTTC | 50  |
|    | AAAAATCTGC ACAGAGGTTT GCTTGAGAAT TTAGCTACAC AAATATGTGT | 100 |
| 35 | AGAAGTGAAA AAAAAA                                      | 116 |

(2) INFORMATION FOR SEQ ID :600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

311

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :600:

ACAGTGTGTG CCCTGTCAGC TCCGCAAATT GGCAGTCACT ACGTTTGTGC 50

CCCCTGTAAC CTTGTGATCT TCACTGCCAC TAGCGATGAA GTCTTCATTA 100

10 TGGCCTC 107

(2) INFORMATION FOR SEQ ID :601:

15 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 173 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :601:

25 ACTGCTAGTG AAATTCACAT GACTCACAAT TCCCTTTAGC CAATGTTACC 50

GAAGTCAGTG TCAAGAAAAC TTAACAGAAA AAAAAAGCA CAGAGTGAGT 100

TCCTACCATA AAAATCCAGG CTGCCCTGTT TCCTAGCTCT AATATAAGCC 150

30 ATTTTCTTTC CTTAGTGAT CAA 173

(2) INFORMATION FOR SEQ ID :602:

35 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

312

## (xi) SEQUENCE DESCRIPTION: SEQ ID :602:

5 GGAAGAGAAC ACATACACGA GGACCAGTAC CTGATGAGGA CAAGAGAGAT 50  
GGGAANNNGC TGTGGAATTC CTTTCGGCAC CCTGGATGTT AACCCCTGCT 100  
CAGGAAAGGG TGCATCTGTC TTCATCATGC CTCTCTCTCC TCCTCCTCCA 150  
GCCACCTCCC AAAGGCAGAG CTGCCGCAAC CTGCCTGGCC ATGTGGTGGC 200  
10 AAGTACCCAG TAGGAG 216

## (2) INFORMATION FOR SEQ ID :603:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 213 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :603:

25 GAAAAACAA TCATGACAGC AACTCTCCTA ACCACAAAA TCACATATGT 50  
TATCTTTCTT TCAGGACTAA TAATTAATAT TTAAGAGGAA AGCACATCAA 100  
TTTCTAGGGC CCTTCTTGGG GAAAGGTTC AATAATTTAG CATACTACA 150  
30 TATTCACTGA ATGCATTCAT ATATTACTAT ATAAACTC TCAGCTACAA 200  
TGTAATATA ATG 213

## 35 (2) INFORMATION FOR SEQ ID :604:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 219 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :604:

5 GACATCTGAT CATCTCACTG GACGCCACAG GGGCAAGAGG GTGGTTTTCC 50  
TGAAGCAGCT GGCTAGTGGC TTATTACTTG TGA CTGGACC TCTGGTCTCA 100  
ATCGAGTTCC TCTACGAGAA CACACCAGAA ATTTGTCATT GCCACTTCAA 150  
10 CAAAATCGAT ATCAGCAATG TAAAAATCCC AAACATCTTA CTGATGCTTA 200  
CTTCAAGAAG AAGAGCTGC 219

## (2) INFORMATION FOR SEQ ID :605:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :605:

25

AGCGAACACG AGCACAGCGA GCGCACAGAG AGCAGCAGGG AGGGCAGCCA 50  
CCGCCGGGAC GCCGGCAGGG GCACGAGAAG GCAAGGAGCG GACACCCGNG 100  
30 NNGA 104

## (2) INFORMATION FOR SEQ ID :606:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :606:

314

.. AATAAAGCAT TCTCACAACC TTTGTTGGGT CAATGATTCC TTTTACCAC 50  
ANNTACAGAA TCTCCACCAT AGCATCA...A CCAACTCTGA GGAAGTTGCG 100  
5 ATAATTCTTA ACTACAAAGA TCCTTCAACA CCCGCATTCT TACAATGTCA 150  
TCGCCGGAAT TTTGAGTGTT CTTTCAATAA CCTACANTA 189

## (2) INFORMATION FOR SEQ ID :607:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :607:

20

GGAAAAGNTC ATTACATAAG CACCAAGNCA TTGATTATGA TCCACCGGAA 50  
GAGCTCGTAT TTATCCTTTG CTTTATNTG AGACCAAGCT AGCCCTGAGT 100  
25 AATTTTANNT GGTTCCTAAA ACATATGGCT TATCGTACTC TAAGAAAAAT 150  
GCCTTACGCA CATTCTTTN T 171

## (2) INFORMATION FOR SEQ ID :608:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 184 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :608:

40

GGAAAAGTNC GCATATAGCG TGCNATAATA CTACGNCTAA GGAGAAACAA 50



315

TTTCCTACAC ATAAAGTAGT GAGAACATCA TCCTATAACA GGGAACTGTG 100

ATTATTTAAA AAACGCAGAA CTTATTTATT TGGCTTTAGA AATAACTGCA 150

5 TACAATGTCA TAAGTCGAAA AGAACTCAAA ATAA 184

(2) INFORMATION FOR SEQ ID :609:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :609:

GGGGACAGCT NNNNNGTTGT TTTGGAGCCT GTTGACTTTG TATTCTCTGC 50

20

CTGTGATTTT CNNTTCTAAA TGAAACTCCA TGTNNNAACC AGGACGAAGN 100

TGAGAAGGAA AACGCCAAAT GCTTTGGTTA TTAGAGNTTA ATAGGNAAGC 150

25 TCTGTTACAC TAGGTGTAGA GTTCCAGAAT GTTCTTTTGT T 191

(2) INFORMATION FOR SEQ ID :610:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :610:

GCAACTGTGC AAACATCCAT CAGTGTGGAG GAATGGTAAA CTGGGTACAT 50

40

GCATGCANTN GNNNCATATT TTTGTGGTTA AGATNNTGAT GTATAGGCAT 100

316

GGAATGTTAT CAAAAGCACA TTAAGTGGTC AAAGCCAGAT ACAGAAGAGT 150

AGGTATGATT TTATAGGNAT AA 172

5 (2) INFORMATION FOR SEQ ID :611:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :611:

TCCACCTTAC AGACCTGATT TGGCTGCTTC TGACGTCTGT TTCCTAATCT 50

T 51

20

(2) INFORMATION FOR SEQ ID :612:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 60 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :612:

CGCCTGAAAC TTTGAGGATA AACTTTTTC AAAAAATAAA ACAGTATCTC 50

35 TTAATCACTG 60

(2) INFORMATION FOR SEQ ID :613:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 75 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

317

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :613:

TTGAAGCTGG GAGGCAGAGG TTGCAGCGTG CAGAGTCGTG CCACTGCACT 50

CCTGGGCGCA CAGCGAGACT GTCTC 75

10

(2) INFORMATION FOR SEQ ID :614:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :614:

ACGGGATTCT CTTCTTCGGC CGCCA 25

25

(2) INFORMATION FOR SEQ ID :615:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :615:

GCAGTGTA CT ATGTTGCGCAT CTGTGAATAG CCACTGCACT CTAGCCTGGA 50

TAATATAGTG AGAACCCATC TC 72

40

(2) INFORMATION FOR SEQ ID :616:

318

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :616:

10

TCTAACTGAT TTCAAAGCAA ACTCTCTCTT AATTAGGCTG CCTCTCCAGG 50  
GGAAATTTAG TGGCAGGGTC CCAGTGAGCC TGTAAGAAGT GTTCTACTCA 100  
CCAGAGTCAC TACTCCAGGT TGAGGACATG AGGCAGG 137

## (2) INFORMATION FOR SEQ ID :617:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :617:

30

GCAGGGCACT CTGGGTGTC AGCCCTCTC CTCTCTGTCC CCTGACACTC 50  
CACAGTGTGC CTGCAACCCA AGTGGCCTTA TCCGTGCAGT GGTGGCAGTT 100  
CAGAAATAAA GGGCCCATTT GAGGGATGAC CGCATTAC 139

35

## (2) INFORMATION FOR SEQ ID :618:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

319

## (xi) SEQUENCE DESCRIPTION: SEQ ID :618:

5 TCTTCTTACT ACACTGGAAG TCTGAACTGG GTGCCTGTTA CCGTCGAGGG 50  
TTACTGGCAG ATCACCGTGG ACAGCATCAC CATGAACGGA GAGGCCATCG 100  
CCTNCNCTGA GGNCGCCAG GCCATTGTTG ACACCNNCAC CTCTCNNCTG 150  
10 ANNNNCCCAA CCAGCCCCAT TNCCAACA 178

## (2) INFORMATION FOR SEQ ID :619:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 73 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :619:

ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC 50  
25 TTCTGCGGCC GCCACCGCGT GGA 73

## (2) INFORMATION FOR SEQ ID :620:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :620:

40 TGCCTTACAC ACTCAGGGAG ACCTCGGGTT GTACCTAGGC CTAGTGGACA 50  
AACTTTGGTA GAGGGTTCGG TACGACTTAC GACACCTGGC CCTACGTCAT 100

320

AGTCCGTACC CTCAGTAACA GTGTAGTAGC TCTTCCTGT

139

(2) INFORMATION FOR SEQ ID :621:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :621:

15 TTCAAAAACA ACTTTATTCA TGACACATAT TAANNNA AAAA CCCCACCCCT 50  
GGAAATGAGC TAAAAAATA AACAAAATCC ACCTCCCACC TCCCTGNCC 100  
CACTTCCTCC CATGCCCTCC AAA 123

20

(2) INFORMATION FOR SEQ ID :622:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :622:

CACCCAAGAC CATCCTTTAT TGTAGTATTA GTTCATGGTA ACTGCATGAA 50  
35 AAAACATTTT NNGAGGAATT TTCAATTTCC AGCTTAAAGA ACNNNCCCAC 100  
CAACATAACC AATTTATGAA ANNNAATTCA TTAAAAGGTA TAGAACCTCT 150  
TGTTNNCATG ATGGCAAGGG ACA 173

40

(2) INFORMATION FOR SEQ ID :623:

321

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :623:

10

TTTATTGTAT CATGAGGCAT TGAAACATCT GAATAAATCA ATGTCTGGGC 50

GGTGAAGGCA GCTGCTTTCT CCTTCACTTC TTTGGGTTAC TAGAGCAACT 100

15

TGTCAGTAGA TT 112

## (2) INFORMATION FOR SEQ ID :624:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :624:

30

ACTCCTTCTG CCCCCGTTCT TCTAGTGAGA GGGGCGGACA AGGGGGCGGC 50

GAAAAGAGGA GAAAGGAGAG AAACAAGAGT CGAGGGGGAC AGGGGAGTCG 100

AGGTCTGCAT CCCCTCCCC 119

35

## (2) INFORMATION FOR SEQ ID :625:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

322

(xi) SEQUENCE DESCRIPTION: SEQ ID :625:

AACAGCACGG AGATTGCGTT TATATATCAG ACCAAGCTC

39

5

(2) INFORMATION FOR SEQ ID :626:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

10

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :626:

CCAGCGCCGA GGTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA

50

20

ATAAAAATCT GAAAACATCC CC

72

(2) INFORMATION FOR SEQ ID :627:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 153 base pairs

25

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :627:

CCTCCGCCGG AGCTATCTGC ACTACATCCG CAAGTACAAC CGTCTTCGAG

50

35

AAGCGCCACA AGAACATGTC TGTACACCTG TCCCCCTGCT TCAGGGACGT

100

CCAGATCGGT GACATCGTCA CAGTGGGCGA GTGCGGCCTC TAGACAAGAC

150

40

AGT

153

(2) INFORMATION FOR SEQ ID :628:



323

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 108 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :628:

10

AAAAGAAGTA GGTCTGTCTG TTCTGGTTGC CCTAAGAGAA GAAGANNNGC 50  
GTGGCCACCT CGAGGTTAAG AGGGATATCA CTCAGCATAA TGTTAAGTGA 100  
CCGGCAGC 108

## (2) INFORMATION FOR SEQ ID :629:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 95 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :629:

30

TCGCACCACT AGAAANCACC GTGACTGAGA AGAATGATGT GACCTTCAGA 50  
CTTGACCCNN GGACAATGNC AGCTCCCAAT GNCCGTCTAG TGGCA 95

## (2) INFORMATION FOR SEQ ID :630:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

324

## (xi) SEQUENCE DESCRIPTION: SEQ ID :630:

CCAGCNCCGA AAAGCCAAGA CTCATCAAC TACATAGGTC TTACCATTGA 50  
5 CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT 100  
AGAAAGGCAT CTTTCGCCAG TGGATTGCC TCAAGGTTG 139

## (2) INFORMATION FOR SEQ ID :631:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :631:

20

CCACCGCCCC GAGCGAATGT AACCCGGCCT TGGACGACCC GACGCCGGAC 50  
TACATGAACC TGCTGGGCAT GATCTTCAGC ATGTNCNNCC TCATGCTTAA 100  
25 GCTGAAGTGG TGTGCTT 117

## (2) INFORMATION FOR SEQ ID :632:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 161 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :632:

CCAGCNCCGA AAAGCCAAGA CTCATGAAC TACATAGGTC TTACCATTGA 50  
40 CCTAAGATCA ATCTGAACTA TCTTAGCCCA GTCAGGGAGC TCTGCTTCCT 100

325

AGAAAGGCAT CTTTCGCCAG TGGATTGCC TCAAGGTTGA GGCCGCCATT 150

GGAAGATGAA A 161

5 (2) INFORMATION FOR SEQ ID :633:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :633:

CCTGCNCCGA CGATGCCAG AATCCAGAAC TTTGTCTATC ACTCTCCCCA 50

ACAACCTAGA TGTGAAAACA GAATAAACTT CACCCAGAAA AACAAAC 97

20

(2) INFORMATION FOR SEQ ID :634:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :634:

CCAGCNCCGA AGCATTGGAT GCTTGACAAA CTAACGGGTG TATTTGCACC 50

35 TCGTCCATCG ACAGGTCCCC AGAAGCTGAG GGAATGTCTT TCCTCTGATC 100

TTCTTCCTCA GGAATAGACT CAAGTATGCG TTGACTGGAG ATGAGGTAAA 150

GAAGATATGT ATGCAACGTT CATTCAAA 178

40

(2) INFORMATION FOR SEQ ID :635:

326

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :635:

10

CTGTCNCCGA TGCACCCGCC ATCCAGCCTG TCCTTTGGAC CACGCCACCC 50  
CTCCAGCATG GTCACCGCCA TGGGTTAGAN CCCTGCTCGA 90

15

## (2) INFORMATION FOR SEQ ID :636:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :636:

CAGGAGACAC AGACAATAGT CACTACATCA CAGCCTTGTT CTTCCGAAG 50  
GATAAAATGT CATTCAAGAA TGGGGTGAGG TGGTTAGAGG GACTAGGTAC 100  
T 101

30

## (2) INFORMATION FOR SEQ ID :637:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

327

## (xi) SEQUENCE DESCRIPTION: SEQ ID :637:

CCGAGCACGA GACCCTGATG CACATTCTAA AATAAAAGAA TGATGCACAT 50  
5 TTAATAAAG CACAGCACAA 70

## (2) INFORMATION FOR SEQ ID :638:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :638:

CCGAGCANAN TCTAACCCGG CCTTGGACGA CCCGACGCCG GACTACATGA 50  
20 ACCTGCTGGG CATGATCTTC AGCATGTGCG GCCTCATGCT TAAGCTGAAG 100  
TGGTGTGCTT GGGTCGCTGT CTACTGCTCC TTCATCAGCT TTGCCAACTC 150  
25 TCGGAGCTCG 160

## (2) INFORMATION FOR SEQ ID :639:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 138 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :639:

CCGAACAAAT GTACGGAATG TGTGAGTCCC TCTGGAGCCC AACATGGATC 50  
40 CGGATCACCT GTTTGAAACC ATCTCCCAAG CCATGCTGAA TGCTGTGGGC 100

328

CGGGATGCAT GTGCAGGCAT GGAGTCATTG TCACATCA

138

## (2) INFORMATION FOR SEQ ID :640:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 80 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :640:

15 CCGACCACCC CTTCCTTTTC TTCGTCCATC CAGCACAGCA AGACCAACGG 50

GATTCTCTTC TGCGGCCGCC ACCGCGTGGA 80

## (2) INFORMATION FOR SEQ ID :641:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 100 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :641:

30

AACTAACTG TTACCTTCCC TCGCTCCACA GAAGAAGACA GCCAGCTTCA 50

GGGGTCCCTG TTGCTGGCCA AGCCAGTGAG CCTGCTGGGA GGCTGGTCCA 100

## 35 (2) INFORMATION FOR SEQ ID :642:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 77 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

329

(xi) SEQUENCE DESCRIPTION: SEQ ID :642:

5 AGAGGACAGA AAGGAACAGA ATGATCTTCC TACNCACAAC ACAAACGTCA 50  
GTTAATGTTC CATCCATGCT GCTTAAA 77

(2) INFORMATION FOR SEQ ID :643:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :643:

20 CCAGCGCCGA GAGCAGCCCC AGTAGCAGCN CATGGCCGGG TCCAACGCCT 50  
ACATCGACAA CCTTCATGGC GGACGGGACC TGTCAGGACN GGCCATCGTG 100  
GGCTACAAGG ACTCGCCCTC CGTCTGG 127

25

(2) INFORMATION FOR SEQ ID :644:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 116 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :644:

GTAGCCAGAC CACAACACCG AGTTGTACCC AGATAGCTGG GATTGGAAGT 50  
40 GAGGAGGTTT CTCACCCAC AGATAACCCA AGACACAAAT GTGCAATTAA 100  
AAGTTTATTT TAGACC 116

330

## (2) INFORMATION FOR SEQ ID :645:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :645:

CCACCACCCG ATTCGTGACC AAGAAGGCTC TGTGCATTTCG GGTTTTCCAG 50  
GAGACTCAAA AGCCGAAGAA GCGAAGAAGA GCCTTAAAGG CTGCAGCAGC 100  
CAGAAAAACA AGCAAAGGAG GAACCCAGAC AGCCCTGCAA AGCATACAAG 150  
ACACTCAAGA CAGCAATTAA TCTGTCATCA TT 182

20

## (2) INFORMATION FOR SEQ ID :646:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :646:

CCAGCGCCGA GGTGTATAT TTCTAGGTGC AGGTATATGA TTGCCATATA 50  
ATAAAAATCT GAAAAC 66

35

## (2) INFORMATION FOR SEQ ID :647:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

40



331

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :647:

CAAGACAATA GTCACATCAT CGCAGCCTTG TTCTTTCCGA AGGATAAAAT 50

GTCATTCAAG AATGGGGTGA GGTGGTTAGA GGGAGTAGGT ACT 93

10

(2) INFORMATION FOR SEQ ID :648:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :648:

CCCCTTTTTG TCCCCACTGA GATGTATGAA GGTTTGGTC TCCCTGGGAG 50

25 TGGGTGGAGG CAGCCAGGGC TTACCTGTAC ACTGACTTGA GACCAGTTGA 100

AAAGTGCACA CCTT 114

(2) INFORMATION FOR SEQ ID :649:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :649:

40

CTGCNCCGAC CACCCCTTCC TTTTCTTCAT CCAGCACAGC AAGACCAACG 50

332

GGATTCTCTT CTGCGGCCGC CACCGCGTGG A

81

(2) INFORMATION FOR SEQ ID :650:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 159 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :650:

15 AGGAGCNCCG ACAAAGACA CATTGGACCT GTCAGCTCCT CTGTTTCACC 50  
AAGCAGACAC AATAACCTTA CCAACAAAGC AGAGTAAGCC AAGTGCCTCT 100  
GTGTGACACC ACCGCATNNT GATGACGCAT AATAAAAATA TAACTAATTT 150  
20 AGACTAGAG 159

(2) INFORMATION FOR SEQ ID :651:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 78 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :651:

35 CCGACCACCC CTCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50  
CTCTTCTGCG GCCGCCACCG CTGGAGCT 78

(2) INFORMATION FOR SEQ ID :652:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 198 base pairs

333

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :652:

|  |     |
|--|-----|
| CCGACAGACG GTCATTGATT ACAACGGGGA ACGCACGCTG GATGGTTTTA | 50  |
| AGAAATTCCT GGAGAGCGGT GGCCAGGATG GGGCAGGGGA TGATGACGAT | 100 |
| CTCGAGGACC TGGAAGAAGC AGAGGAGCCA GACATGGAGG AAGACNATGA | 150 |
| TCAGAAAGCT GTGAAAGATG AACTGTAATA CGCAAAGCCA GACCCGGG   | 198 |

(2) INFORMATION FOR SEQ ID :653:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :653:

|  |     |
|--|-----|
| CCGAAAAGCC AAGACTTCAT GAACTACATA GGTCTTACCA TTGACCTAAG | 50  |
| ATCAATCTGA ACTATCTTAG CCCAGTCAGG GAGCTCTGCT TCCTAGAAAG | 100 |
| GCATCTTTCG CCAGTGGATT CGCCTCAAGG TTGAGGCCGC CATTGGAAGA | 150 |
| TGAAAAATTG CACTCCCTTG GTGTAGACAA TACCAGTTCC ATTGGTGTTG | 200 |
| TTGCTATAAT AACACTTTTC TTTT                             | 224 |

(2) INFORMATION FOR SEQ ID :654:

40

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 226 base pairs

334

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :654:

CCGCCTCAGA CTCTGGACCA GCCACTGTCC CAGAAGCCAG GCCGGGCAGT 50  
GGCCTTCTCC ACTCCCCTCT GACTTCTCCA AGGGGCTCAG TGGCCAGTGC 100  
CCCCCAGGAG GCTCCACCCT CAACTCAACC CAAGCAAGAG GGACAGATGA 150  
AAAACAAAAT CCAATCAGGG CGATAAATGG CGGGGGGTTT AATTGGTTT 200  
CTGAGCGCAT AAAGCTAAGG AGGGGT 226

20

## (2) INFORMATION FOR SEQ ID :655:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :655:

30

TTAAAAAAT TCCCCCTTT AATTGACCAA AGTAAAGCCA TGACATTTCA 50  
TTTGTAACC TGTTTAGAAT TATAAAATC ATTCATTTG GCCCAGCCCA 100  
TACGCCCAAG AGAAACTTC CAGACTTTTC TGATGCCATC CAGTTTTGTT 150  
CTTACAAAAT GCATATT 167

40

## (2) INFORMATION FOR SEQ ID :656:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

335

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :656:

CCACCCCTTC CTTTCTTCA TCCAGCACAG CAAGACCAAC GGGATTCTCT 50  
TCTGCGGCCG CCACCGCGTG GA 72

10

(2) INFORMATION FOR SEQ ID :657:

15

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 178 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :657:

AGAGGGTTTT CTATATGTAA TTCTTTTATT CTGTAAAAGG TAACAAAATA 50  
TACAGAACAA AAAAAGTTTC CCTTTTAAA ACTAATGTTA CAAATCTGTA 100  
TTATCACTTG TATATAAATA GTATATAGCT GATCATTAAAT AAGGTGTATA 150  
GTACAATGTA TTCTAAAGT GTCCGCC 178

30

(2) INFORMATION FOR SEQ ID :658:

35

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 76 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

336

(xi) SEQUENCE DESCRIPTION: SEQ ID :658:

CCGACCACCC CTCCTTTTC TTCATCCAGC ACAGCAAGAC CAACGGGATT 50  
5 CTCTTCTGCG GCCGCCACCG CGTGGA 76

(2) INFORMATION FOR SEQ ID :659:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :659:

GCCAGCGCCG AGGTGCGATA TTTCTAGGCG CAGGTATATG ACTGCCATAT 50  
20 AACAAAAACC NTGAAAAC 68

(2) INFORMATION FOR SEQ ID :660:

(i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :660:

35 CCCAACTTC TTAAAAATC AAGTAATGTT TACAAGAAAG AATAAAATCT 50  
TAATCCTTTT CACTTTTAAA GACAATCAGA TAAGATTACC CACTGCGATT 100  
AAACACTGAT CAAACTCAGT TGTCTTACG TTAGCATTAC TCTGTCATAG 150  
40 C 151

337

## (2) INFORMATION FOR SEQ ID :661:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :661:

AGGCACTGAC CCCTGCCACC CCTCACTGCA TTAAC TTCAG CCACGTCTCC 50  
TCCTTCCTCT GCGCTTCCAG TGATAAGGGT ACTGTCCATA TCTTTGCTCT 100  
CAAGGATACC CGCCTCAACC GCCGCTCCGG CCTGGCTCGC GTGGGCAAGG 150  
TGGGGCCTAT GATTGGGCAG TACGTGGACT CTCAGTGGAG CCTGGCGAGC 200  
TTCAGTGTGC CTGCTGAGTC AGCTTGCATC TGCGCCTTCG GTGCG 245

## (2) INFORMATION FOR SEQ ID :662:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :662:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50  
AATAAAAACM TGA AACACC CC 72

## (2) INFORMATION FOR SEQ ID :663:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs

338

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :663:

GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTGCCTAT CACTCTCCCC 50  
10 AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :664:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :664:

25 GCCTGCGCCG ACAAACAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCCG 50  
GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC 100  
CCCCACCTGC TGTTCATATG ACCCAGGGGG CGCACACTAC CCCACAGGCG 150  
30 CGCCCATACA GACATTCACC GGAGCCGGCT GCTGCGAACT CGACCCCGTG 200  
CGGATAGTCA CACTCCCTGC CGA 223

35 (2) INFORMATION FOR SEQ ID :665:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



339

(xi) SEQUENCE DESCRIPTION: SEQ ID :665:

5 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50  
AATAAAAATC TGAAACACC 70

(2) INFORMATION FOR SEQ ID :666:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :666:

20 GCCAGCGCCG ACCGCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA 50  
TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAAA CCAACCACC 100  
TTTCTACGTA CCGTATAG 118

25

(2) INFORMATION FOR SEQ ID :667:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :667:

GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTGCCTAT CACTCTCCCC 50  
40 AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :668:

340

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 59 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :668:

10

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTTGATCTTC AACTCTGCAT 50  
ACAAGCAGA 59

## (2) INFORMATION FOR SEQ ID :669:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :669:

25

GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA 50  
CATGGATCCG GATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG 100  
CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150  
GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC 200  
CTGCTCCCAG AGCCCACTTT TTT 223

35

## (2) INFORMATION FOR SEQ ID :670:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

40

341

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :670:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC

37

(2) INFORMATION FOR SEQ ID :671:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :671:

20

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC

37

(2) INFORMATION FOR SEQ ID :672:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 59 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :672:

35 GCCACCGCCG ACTCCAGGCA CTCACTCAAA CTCGATCTTC AACTCTGCAT

50

ACAAGCAGA

59

(2) INFORMATION FOR SEQ ID :673:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs

342

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :673:

|    |            |            |            |            |            |     |
|----|------------|------------|------------|------------|------------|-----|
|    | GCCTGCGCCG | ANGCATTCCC | TTTGACCTGA | GTCTGCAGCA | GGTCCCTTTT | 50  |
| 10 | GCGCTTCCTT | CCCCTCAGGT | AGCCTCTCTC | CCCCTGGGCC | ACTCCCGGGG | 100 |
|    | GTGAGGGGGT | TACCCCTTCC | CAGTGTTTTT | TATTTCCGTG | GGGCTCACCC | 150 |
| 15 | CAAAGTATTA | AAAGCAACTT | TGCAATT    |            |            | 177 |

## (2) INFORMATION FOR SEQ ID :674:

20

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 77 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :674:

|    |            |             |            |            |            |    |
|----|------------|-------------|------------|------------|------------|----|
| 30 | GCCTGCGCCG | AGCACAAAGAC | AATGACGAAC | ATTTTAAAAA | AAAAGAATGA | 50 |
|    | CGCACATTTT | AATAAAGCAC  | AGCACAA    |            |            | 77 |

## (2) INFORMATION FOR SEQ ID :675:

35

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 176 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: double
  - (D) TOPOLOGY: linear

40

343

## (xi) SEQUENCE DESCRIPTION: SEQ ID :675:

50  
GCCAGCGCCG ACACCCAGAG ACTACAGTAC TTAGGGGTTA CACACAACAG  
5 CCGTAACTGG CGGCTATCTG TTCATAACAA ACAAACCATA GCATATTTAC 100  
ACCGCATCAC ATCGAGTGAT TATAGAAATC CATAACACA CCGATTGCAT 150  
AAAATCTTTT TTTAGGAAAA AAACAC 176

10.

## (2) INFORMATION FOR SEQ ID :676:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 141 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :676:

50  
GCCAGCGCCG ACGCCCAGAG AATACAGTAC TTAGGGGTTA CACACAACAG  
25 CCGTAACTGG CGGCTATCTG CTCATAACAA ACAAACCACA GCATATCTAT 100  
ACCGTATCAC ATCGAGTGAT TATAGAAATC CACAGAGAGA C 141

30

## (2) INFORMATION FOR SEQ ID :677:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 365 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :677:

50  
CTCTGAACAG ACACGAAGCT GCCCCTCGTA CAGCCACTCG GGCGCTGACC

344

ACCAGGGAAG GCAAAGGCAT AGGACTTCCA CACAGTCCAG ACACTGCACG 100  
CTGACAAGCG CCTCCGCGGC GGCTGCGAGC CGGACTCAGG CGGATCTTGA 150  
5 CAGCCTTGCC CGCGAGTGCC CGGGGATAGA ACCCGTGCCG GTGGACCTAG 200  
GTGACTGGGA GGCCACCAAG CAGGCACTGG GCAGCGTGGG CCCCCTGGAC 250  
CTGCTGGAGA ACAACACCAC CGTCGCCCTG CCGCAGCCCT TCCAGGAGGT 300  
10 CACCAAGGAG GCCTTCGACA GATCCTTTGA GGTGAGCTTG CGTGCGATCA 350  
TCCAGGTGCT GTAGA 365

15 (2) INFORMATION FOR SEQ ID :678:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 366 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :678:

GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC 50  
CAGGGAAGGC AAAGGCATAG GACTTCTGCA CGGTCCAGAC CCATGTACGC 100  
30 GACGGGCGCC TNCGCGGTGG CTGCGAGCCG GATTCAGGCA GATCTTGACA 150  
GCCTTGCCCCG CGAGTGCCCCG GGGATAGAAC CCGTGTGCGT GGACCTNGGG 200  
TGACTGGGAG GCCACCAAGC AGGCACTGGG GTAGCATGGG CCCC GCGGAC 250  
CTGCCGGAGA ACAATACCAC CGCCGCCTNT GCCGCAGTCT TTCCCGGAGG 300  
TCACCAAGGA GGCCTNTTGA TAGATCTTTT GAGGTGAGCT TGCCTGCGGT 350  
40 CATCTAGGTG CTGTAG 366

345

## (2) INFORMATION FOR SEQ ID :679:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :679:

GCCTGCCCCG ACACGAAGAT GACCCTCGAC AGCCGCCGGG CGCTGATCAC 50  
CAGGGAAGGC AAAGGCATAG GCCAGCACCG ATGAATTCCC TTTGACCTAA 100  
GTCTGCAGCA GGCCCCTTTT GCGCTTCCTT CCCCTCAGGC AGCCTCTCTC 150  
CCCCCGGGCC ACTCCCGGGG GCGAGGGGGT TACCCCTTTC CCAGTGCTTT 200  
TTATTCCCGC GGGGCTCACC CCAAAGCATT AAAAGCAGCT TTGCAATTCC 250  
TTG 253

## 25 (2) INFORMATION FOR SEQ ID :680:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :680:

GCCAGCGCCG AGGCTTCTCC TAGGGCTGCT CCTGGGCCTA GCTCTTACAG 50  
GCTCGTCCCC CAGGCCTGCC CTTCTCCACT GCCCCCTCCC GTGCCTGGGC 100  
CCACACACCC TTCAGGAAGG GGGAGCACTG AGAAGCACAG CACAGGGGCT 150

40

346

CAGCCTGGGA TCCGGTGACG GCCTAGGCAG AGGCTGGGCC AGGAGTCCCA 200  
AAGGTCAGTG ACAGTTTCTC AGAAGGGGCC CAGCGTCCAC CTCTCTCCCA 250  
5 GGACCAGACA CCCCTTCCAG GCTCCCCCAC CCCCCTACGG GCTC 294

## (2) INFORMATION FOR SEQ ID :681:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 268 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :681:

CCGCCAAGTG ACACCAAAGC CCTGGTTGAC TTTGACAGCC CCGTGGGCGC 50  
20 GCGGGAGGCC GGGCACTCTA GGGTCTACCT ACCAGTGCAA TCGTTTAGCG 100  
CTTTTTCAGT GGGGCAGGGC AGGAAGCAGG CGGGACCAGG CAGCCAGTTC 150  
25 TCAAAGGCTG CGGGGCCAAC TAGAGGCCAC AGCCCCTCAC CCCTAGACAC 200  
TGCCAACCAG AACTGACACG CGACCTCCTG GGCGCTGACG CCATTAAAC 250  
CAACGTTGGC GCCCGGCG 268

30

## (2) INFORMATION FOR SEQ ID :682:

(i) SEQUENCE CHARACTERISTICS:  
35 (A) LENGTH: 354 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :682:



347

GCCACCGCCG AGGAAAACCG TGCCTGTGA GCCATGATCA ACCCCACCGT 50  
 GCTCTTCGAC ATTGACATCG ACGGCTGAGC CCTTGACCTA GTCTCCTTTG 100  
 5 AGCTGTTTGC AGACAAGGTC CCAAAGACAG CAGAAAATTT TCGTGCTCTA 150  
 AGCACTGGAG AGAAAGGATT TGGTTATAAG GGTCCTGCT TTCACAGAAT 200  
 TATTCCAGGG TTTATGCGCC AGGGTGGTGA CTTACACGCG CATAATGGCA 250  
 10 CTGGTGGCAA GTCCATCCAT GGGGAGAAAT TTGAAGACGA GAACTTCATC 300  
 CTAAAGCATA CGGGCCCTGG CATCTTGCCC ATGGCAAATG CTGATCCTGA 350  
 15 TACA 354

## (2) INFORMATION FOR SEQ ID :683:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 148 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :683:

CCTCTCCGTG AGGACAGGGC AGTCTTGGTG CGCAGCCCCT CTCCTCTCTG 50  
 30 TCCCCTGACA CTCCACAGTG CGCCTGCAAC CCAGGCGGCC TTATCCGCGC 100  
 AGTGGCGGCA GTTCAGAAAT AAAGGGCCCA TTTGCGGGAT GCCGCATT 148

## 35 (2) INFORMATION FOR SEQ ID :684:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 307 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: double  
 (D) TOPOLOGY: linear

348

## (xi) SEQUENCE DESCRIPTION: SEQ ID :684:

5 AGCACCGAGG CGCTCAAGGT CCTGGGGAAC CCCAAGAGCG ACGAGACGAA 50  
CGCGAAGGCG CTGGACTTTG AGCACTTTCT GCCCATGCTG CAGACAGTGG 100  
CCAAGAACAA GGACCAGGGC ACCTATGAGG ATTATGCCGA AGGACTTCGG 150  
10 GCGCTTGACA AGGAAGGAAA TGGCACCCTC ATGGGCGCTG AAACCCGGCA 200  
TGCTCTTGCC ACACTGGGCG AGAAGACGAC AGAGGAAGAA GCAGAGACGC 250  
TGGCGGCAGG GCATGAGGAC AGCAATGGTT GCATCAACTA CGAAGCATTT 300  
15 GTGAGGC 307

## (2) INFORMATION FOR SEQ ID :685:

20 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 174 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :685:

30 CCATCTCAAG GCGATCCATG GAAAGCTTCC TGGGGAACGT ATGCTAGCAG 50  
AGCTTCTCCC CGTGAATCAC ATGCCGGAGA TCCCACTCTT AGCTGGCAAA 100  
TGAATCCGAA TTGACACAGC AGCCCCATAA GCATCAGCCC TGTAGAGTGA 150  
35 GGAGCCATCT CTAGCGGGCC CTTC 174

## (2) INFORMATION FOR SEQ ID :686:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 106 base pairs  
(B) TYPE: nucleic acid

349

(C) STRANDEDNESS: double

(D) TOPOLOGY: lin ar

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :686:

ACATGCCAAA GAAAGCGTGC ATATTAGCCT ATAGAACCAC AGTAATCACA 50

10 CTAGAGAAAT TCCACTGCTA CAATAAAATG TAATCGGAAG CATCTTTACT 100

TATAAA 106

15 (2) INFORMATION FOR SEQ ID :687:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

20 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :687:

CAGATTTTTT TCAATTCTCC ACCCGCCAAA AGGGGAAGGG CTTTCCCCCA 50

GAGAAAAGGA AAGGGGGGAA AAGGGGAAAA AACCCAACCC AAAACCA 97

30

(2) INFORMATION FOR SEQ ID :688:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 172 base pairs

35 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :688:

350

GCCTCTCTCT GGGCAAGTTC ATGGCTTCTG TGAGCCCTTT NACTGACCTC 50  
CAGACACTGT TAGGCTGGAG CCTCGGTAGC CGTTCCTCCT GCCCACTGGA 100  
5 CCTTCCAACA GGCCCTCCTC CCCTCCTTGA ACCGGCCCTT CCTGGCCTTT 150  
GAATAGAGTC TAAGCGAACG AC 172

## (2) INFORMATION FOR SEQ ID :689:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :689:

20

GCCACCGCCG AGCTCACCCC TCGGGTGCAC GCCTTCCTTG GACAAGTTTT 50  
TGGCTTCTGC GAGCCTTTTA CTGACCTCCA AACGCTGTTA AGCCGGAGCC 100  
25 TCGGTAGCCG TTCCTCCTGC CCACTGGACN TCCCAACGGG CCCTCCTCCC 150  
CTCCTTGAAC CAGCCCTTCC TGGCCTTTGA ATAAAGTTTA AGCGAGTAGC 200

## (2) INFORMATION FOR SEQ ID :690:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :690:

40

GCCACCGCCG AGCAGCAGCT TACAGCCAGG GCAGCTTTGA ATGCGGCCCA 50

351

ACACAAATTC ACAAGTGNTC TCAAAAAACT C

81

(2) INFORMATION FOR SEQ ID :691:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :691:

15

TTCCTAACCG ATCGAATGAA GGATTCAAAA TTAACCACTC CAAGGGGGGA

50

TTGAAGGAAG AACCCTCTT AACGGACAAA AAGAAAGAAA GGGGAGGGAG

100

TAACAGGGAT ATGAGCTCTA GCCGCCCAAG CTAGCAATGG CAACCCTTCT

150

20

GGGTCCCCTT TCAGCATGCG GAAGCTTTTC TTCGACTTCA CTCCATAAAC

200

AGCTGACGCT CAAAAG

217

25

(2) INFORMATION FOR SEQ ID :692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :692:

CGGCCTTCTG GAAACCCATG AAAAAAAAAA GTCCGCACC TCCAAGGGGA

50

GAAGAGTAAG AGACAGCTTT CA

72

40

(2) INFORMATION FOR SEQ ID :693:

352

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :693:

10

TCTGCTGCCG CCCGCAAGCA GAGGGACTCG GAGATCATGC AGGGGAAGCA 50  
GAAAAAGGCA AACAGAAGA AGGAGGAACC CAAGCAGCTT TCGGGCTTCG 100  
CGTCCAACCC TCTTGCCCTT CACCTACGCG CCTAGAGCCA GTCCCACCAC 150  
GCTCGCGTTT CCTCCTGTAG CGCTCACAGG CCCCAGCACC GATGGCATTC 200  
CCTTTGACCT AAGCCTACAG CAGGCCCTT TTGTGCTTCC TTCCCCTCAG 250  
GCAGCCTCTT TCCCCCTGGG CCACTCCCGG GGGTGAGGGG GTGTCTCTTC 300  
CCGATGCTTT TTGTTACCGT GGGGTTTGC 329

25

## (2) INFORMATION FOR SEQ ID :694:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :694:

TCTGCTGCCG CCCGCAAGCA GAGGGACTCG GAGATCATGG CCTGCGCCGA 50  
ACAAATGTAC GGAATGCGTG AGTCCCTCTG GGAGGCC CACGGATCCG 100  
GATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG CTGCGGACCA 150

40

353

GGATGCAGTG TCAGGCATGG GAGTCATTGC CCACATCATC GAGAAGGACA 200  
AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTAACC CTGTTCCCAG 250  
5 AGCCCACTTT TTTTTTTTTT TTGGAATAA AATAGCCTAT CTTTCG 296

## (2) INFORMATION FOR SEQ ID :695:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 211 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :695:

GCCAGCACCG ACCTAGCCTA AGCCGTCTAG AACCACCTAA GCCCCTAAGG 50  
20 AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGCAGAGG 100  
CGTGTCTTAG CACTAACCTC CTCCCTAGCC CCTTATTGG TGGCAGAAGT 150  
25 GGCCTCCACC CCTTCACCGT TAAAAATAC TCCGTGGAGA AAAGAAAGCT 200  
TNAAGGAGTA G 211

## (2) INFORMATION FOR SEQ ID :696:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 92 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :696:

40

GCCTGCACCG ACAATGCCCA GAACTCCAGA ACTTCACCTA TCACGTATCC 50

354

CCAACAACAC AGACGGCGAA AACAAAACAA ACTTAAACCT AG

92

## (2) INFORMATION FOR SEQ ID :697:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 314 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :697:

15 GCCAGCACCG AGGCCTAGGG TAGAGCAGAC TGTGGCTTTA CCTCGGTGTC 50  
CTACCAGCAA GGGGTCCTAT CTACCACCAT CCTCTATGAG ATCCTGCTAG 100  
GGAAGGCCAC CCTGCATGCT GCGTTGGTCA GCACCCTTGC GCTGATGGCC 150  
20 ATAGTCAAGA GAAAGGATTT CTGAAGGCAG CCCTAGAAGC GGAGTTAGGA 200  
GCTTCTAACC CGTCATGGTT TAAATACACA CCCTTTTTTG GACAGCGCTT 250  
25 CTGAAGAGCT GCTCTTACCT CTCTGCATCC CAATAGATAT CCCCCTATGC 300  
GCATGCGTAC CTGT 314

## (2) INFORMATION FOR SEQ ID :698:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 198 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :698:

40 GCCACCGCCG AGTTCACCCC TGCAGTGCAC GCCTCCCTGG ACAAGTTCCT 50



355

GGCTTCTGTG AGCACCGTGC TGACCTCCAA ACACCGTTAA GCTGGAGCCT 100  
CGGTAGCCGT TCCTCCTGCC CACTGGACTC CCAACAGGCC CTCCTCCCCT 150  
5 CCTTGCACCG GCCCTTCCTG GTCTTTGAAT AAAGTCTAAG CGGGCAGC 198

## (2) INFORMATION FOR SEQ ID :699:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 230 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :699:

GCCAGCACCG ACAGCAACAA AAATGTTCCC ACAGAGATCA GGATGACTTG 50  
20 CTGAAGCTCA GTGGAGGCTA AAAAGAGGAC ACAAAAGTGA ACAGAATGAC  
CTTCCTACGC ACAACACAAA CACCAGTTAA TGCTCCATCC ACGCTGCTTA 150  
25 AAGAGCATTC CTGTCCTAGC AAAATGGGCA AGTCCCTCTA CCCCCCACCC 200  
TTAGCCGGCA TGCTTACATT AATAGCTAGA 230

## (2) INFORMATION FOR SEQ ID :700:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 282 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :700:

40

AGCAACAAAA ATGTTTCCAC GGAGATCAGG ATGACTTGCT GAAGCTCAGT 50

356

GGAGGCTCAA AAGAGGACAC AAAAGTGAAC AGAATGATCT TCCTACGCAC 100  
AACACAAACA TCAGTTAATG CTCCATCCAC GCTGCTTAAA GAGCATTCCT 150  
5 GTCCTAGCAA AATGGGCAAG TCCCTCTACC CCCACCCCTC ACTTGGCATG 200  
CTTACATTAA TAGCTAAAGT CAATCCTGTA ATGAAATAAA GCAAATGGCA 250  
GCTGTCTAGT AGCCTCCACT ACCGCAAATA TC 282

10

(2) INFORMATION FOR SEQ ID :701:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :701:

GCCTGCGCCG AACAAACGCA CGGAATGAGC GAGTCCCTCT GGGAGCCCAA 50  
25 CATGGATCCG AATCACCTGT TTGAAACCAT CTCCAAGCC ATGCTGAATG 100  
CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150  
GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTAACC 200  
30 CTGTTCCCAG AGCCCACTTT TCCCCTATTT TGGAAATAAA ATAGCCTGTC 250  
TTTCG 255

35

(2) INFORMATION FOR SEQ ID :702:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

357

(xi) SEQUENCE DESCRIPTION: SEQ ID :702:

5 GCCTGCGCCG AGCACAAGAC AATGATGAAC ATTCTAAAA AAAAGAATGA 50  
CGCACATTTT AATAAAGCAC AGCACAAACT GTTCTTTCC 89

(2) INFORMATION FOR SEQ ID :703:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 96 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :703:

20 GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGCCGC ACCCCCGCTA 50  
GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GTCGGG 96

(2) INFORMATION FOR SEQ ID :704:

25

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :704:

35

GCCTGCGCCG AACAAACATA CAGAACGCAA CGAGTCCCTC TGAAGGCCCA 50  
ACACGGATCC GAATCACCTG GCCCCAAACC ACCTACCTAG CCATGATGAA 100  
40 TGCTGAGGAC CCAGATGCAG TAC 123

(2) INFORMATION FOR SEQ ID :705:

358

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 262 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

5 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :705:

10 GCTTGATGCC TGCGCCGAAC AAACATACAG AATGCGGCGA GTCCCTCTGG 50  
ACGCCCAACA CGGATCCGGA TCACCTATCT GAAACCATCT CCCAAGCCAT 100  
15 GCTGAATGCT GCGGACCAGG ATGCAGTGCC AGGCATGGGA GCCATTGCCC 150  
ACATCACCGA GAAGGACAAA ATCACCACCA GGACACTGAA GGCCCGAATG 200  
GACTAACCTT GTTCCCAGAG CCCACTTTTT TTCTTTTTC AATAAAAC 250  
20 AGCCTGTCTT TC 262

## (2) INFORMATION FOR SEQ ID :706:

## 25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 209 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :706:

35 GCCAGCACCG ACCTAGCCTA AGCCGTCTAA AACCACCTGA GCCCCTGAGG 50  
AAACCTGTGG TCACACTGGG CCCTCCTCAG GAACTCTCCC TGCGCAGAGG 100  
CGTGTCTTAG CACTGCCCCC CTCCCTAGCC CTTATTTGG CGGCGGAAGC 150  
40 GGCTCCACC CTTCCCTGT TTGCAACAC TCTGCGGAGA AAAGAGGACT 200

359

TCAGGGAGT

209

## (2) INFORMATION FOR SEQ ID :707:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 170 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :707:

15 GCCAGCACCG AGATGACGAG CTTTCTGCTG CCACCCACAA GCAGAGGGAC 50  
TCGGAGATCA CGCAGCAGAA GCAGAAAAG GCAAACAAGA AGAAGGAGGA 100  
ACCCAAGCAG CTTTGCGGCT TCACGCCCAA CCCTCTCGCC CTCACCTGT 150  
20 GAGCCTGGAG CCAGTCCCAC 170

## (2) INFORMATION FOR SEQ ID :708:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 160 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :708:

35 GCCACCGTCG AGGATTGAGC AGCCTCCCCC TTGAGCCCCC TCACTTCCCG 50  
ACGTTCGGTT TCCCCCTGCC CGCCTTTTTC CGCCACCACC GCCGCCGCCT 100  
TCTGCAGGCC GTTTCACCG AGGAAAAGGA ATCGTATTGT ATACCCGCTA 150  
40 CCCAGAACCT 160

360

## (2) INFORMATION FOR SEQ ID :709:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 51 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :709:

GCCAGCACCG AGCAACCTGG GTCCAAATAA AACTAAACT GCAAACTCCT 50  
15 G 51

## (2) INFORMATION FOR SEQ ID :710:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :710:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50  
30 CAGGATTCTC TTCT 64

## (2) INFORMATION FOR SEQ ID :711:

35

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 104 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

361

(xi) SEQUENCE DESCRIPTION: SEQ ID :711:

CCAGCCAAAG ATTCCCAGGC TTTCTTGTCT CAGCAACTTT CCCATCTTCT 50  
5 CTCTCTTGGA TGATGTTTGC CGTCAGCATT CACCAAATAA ACTTGCTCTC 100  
TGGG 104

(2) INFORMATION FOR SEQ ID :712:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :712:

20

CTAGAAATAG ACCCACAATT TAGAGACAAT CTATACTAGA TTTATCTCCT 50  
TTGTTTTTAG TTGAAGGC 68

25 (2) INFORMATION FOR SEQ ID :713:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :713:

AGCGAATGTA AGGGGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT 50  
GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT 100  
40 GTGCTTGGGT CGCTGTCTAC TGCTCCT 127

362

## (2) INFORMATION FOR SEQ ID :714:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 90 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :714:

CTTGGGAGAT AACAGTTTCC CCTCTCCCTC CCCCTGCAGA TTTCCAGCGC 50  
15 CCGGACCAAG GCCAAGTAAG CCTCTACAAA CCTAGCATTT 90

## (2) INFORMATION FOR SEQ ID :715:

## (i) SEQUENCE CHARACTERISTICS:

- 20 (A) LENGTH: 69 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :715:

CCAGCGCCGA GGTGTATAT TTGTAGGTGC AGGCACACGA CCAGGACACA 50  
30 ACAAAAATCT GAAAACATC 69

## (2) INFORMATION FOR SEQ ID :716:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 102 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40



363

(xi) SEQUENCE DESCRIPTION: SEQ ID :716:

GCCGAGGAGA ACCCCCGCTC CCTGAGGAGG ACCTGTCCAA ACTCTTCAA 50  
5 CCACCACAGC CGCCTGCCAG GATGGACTCG CTGCTCATTG CAGGCCAGAT 100  
AA 102

(2) INFORMATION FOR SEQ ID :717:

10

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 124 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :717:

20

AGCGAATGTA ACCCGGCCTT GGACGACCCG ACGCCGGACT ACATGAACCT 50  
GCTGGGCATG ATCTTCAGCA TGTGCGGCCT CATGCTTAAG CTGAAGTGGT 100  
25 GTGCTTGGGA TACGCTGTCT ACAG 124

(2) INFORMATION FOR SEQ ID :718:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 123 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :718:

40

GGAAAACCGT GTACTATTAG CCATGGTCAA CCCCACCGTG TTCTTCGACA 50  
TTGCCGTCGA CGGGAGCCCT TGGCGCGCGT CTCCTTTGAG CTGTTTGAC 100

364

ACAAGGTCCC AAAGACAGCA GAA

123

## (2) INFORMATION FOR SEQ ID :719:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 54 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :719:

15 ACCACCCCTT CCTTTCTTC ATCCAGCACA GCAAGACCAA CGGGATTCTC 50

TTCT 54

## (2) INFORMATION FOR SEQ ID :720:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 117 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :720:

30

GACCACAGGG CCTTCAATCC TTTTTGTTT TCAACAGTCT TGCTGAATTA 50

AGCAGAAAGG GCCTTGAATC CTGGCCTGGA ATTTGGGCAG ATATAGCATT 100

35 AATAAACTG TGCACTC 117

## (2) INFORMATION FOR SEQ ID :721:

40

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: doubl

365

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :721:

GACCACCCCT TCCTTTTCTT CATCCAGCAC AGCAAGACCA ACGGGATTCT 50

CTTCT 55

10

(2) INFORMATION FOR SEQ ID :722:

(i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 92 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :722:

GACTTCACGA ACTACACAGG TCTTACCATT GACCTAAGAT CAATCTGAAC 50

25 ATTCTTAGCC CAGTCAGGGA GCTCTGCTTC CTAGAAAGGC AT 92

(2) INFORMATION FOR SEQ ID :723:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 55 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :723:

TATTTCTAGG TGCAGGTATA TGATTGCCAT ATAATAAAAA TCTGAAAACA 50

40

TCCCC 55

366

## (2) INFORMATION FOR SEQ ID :724:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 164 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :724:

GTGTACTATT AGCCATGGTC AACCCCACCG TGTTCTTCGA CATTGCCGTC 50  
15 GACGGGCGAG CCCTTGGCGC GCGTCCTTTG AGCTGTTTGC AGACAAGGTC 100  
CCAAAGACAG CAGAAAAATT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA 150  
TTTGTTTATA AGGG 164

20

## (2) INFORMATION FOR SEQ ID :725:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 110 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :725:

GTGAGAAGCT GCAGCGGTGA CCTGGAGGCT GCGATGTGGA GGTGGAGGAC 50  
35 ACACCCTCAA CCGTTGCTCC TGTAGCTTCC GAGTCCTGGT GGTGTCGGCC 100  
AAGTTCAGTA 110

40

## (2) INFORMATION FOR SEQ ID :726:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 base pairs

367

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :726:

|  |     |
|--|-----|
| CCGTGTACTA TTAGCCATGG TCAACCCAC CGTGTTCTTC GACATTGCCG  | 50  |
| TCGACGGGAG CCCTTGGCGC GCGTCTCCTT TGAGCTGTTT GCAGACAAGG | 100 |
| TCCCAAAGAC AGCAGAAAAT TTTCGTGCTC TGAGCACTGG AGAGAAAGGA | 150 |
| TTTGGTTATA AGG   | 163 |

10

15

## (2) INFORMATION FOR SEQ ID :727:

## (i) SEQUENCE CHARACTERISTICS:

20

- (A) LENGTH: 105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :727:

30

|  |     |
|--|-----|
| GAGGGCGAGT TCGAGGAGGA GGCTGAGGAG GAGGTGGCCT AGAGCCTTCA | 50  |
| GTCAGTGGGG AAAGCAGGGA AGCAGTGTGA ACTCTTTATT CACTCCCAGC | 100 |
| CTGTT  | 105 |

35

## (2) INFORMATION FOR SEQ ID :728:

## (i) SEQUENCE CHARACTERISTICS:

40

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

368

## (xi) SEQUENCE DESCRIPTION: SEQ ID :728:

5 GCCAGCGCCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG 50  
ACCTAAGATC AATCTAAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCCT 100  
AGGAAGGCAT CTTTCGCCAG TGGATTCGCC TCAAGGTCTGA GGCCGCCACT 150  
10 GGAAGACGAA AAATAGAACT CCCTTAGAGT AGACAA... 186

## (2) INFORMATION FOR SEQ ID :729:

## (i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 167 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :729:

25 GCCAGCGCCG AGGTTGCATA TTCTAGGCCG AGGTATATGA TTGCCATATA 50  
ATAAAACCT GAAACATCC CACCCGGGAA AAAAAAAAAA AAAAAAAAAA 100  
AAAAACACCC CCCCCCACA AAAAATCAA ATTCCCCTCC CAAAAACCC 150  
30 CCTCAAAATC AAAAAAC 167

## (2) INFORMATION FOR SEQ ID :730:

## (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :730:

369

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

CAGGATTCTC TTCT 64

5 (2) INFORMATION FOR SEQ ID :731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :731:

GCCAGCGCCG AGACCCTGGC GGCCTACCGG CCCCCGTGC ACCCCCGCTA 50

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

20

(2) INFORMATION FOR SEQ ID :732:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :732:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50

35 CAGGATTCTC TTCTGCAGCC GCCACCGCGT CGGA 84

(2) INFORMATION FOR SEQ ID :733:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 96 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

370

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :733:

GCCAGCGCCG AGATCCTGGC GGCCTACCGG CCCTCAGTGC ACCCCCGCTA 50

GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

10

(2) INFORMATION FOR SEQ ID :734:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 96 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :734:

GCCAGCGCCG AGATCCTGGC GGCCTACCAG CCCTCCGTGC ACCCCCGCTA 50

25 GCGCCCCACC CCGCGTCTAT CGCCCAATAA AGGCATCTTT GCCGGG 96

(2) INFORMATION FOR SEQ ID :735:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 97 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :735:

GCCAGCGCCG AGATCCTGGC GGCCTACCAG CTCCTCAGTG CACCCCACT 50

40 AGCACCCAC CCCGCACTA TCGCCCAATA AAGGCATCTT TGCCGGG 97



371

## (2) INFORMATION FOR SEQ ID :736:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 127 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :736:

GCCAGCGCCG ACCACAGGGC CTTGAATCCT TTTTGTTTT CAACAGTCTT 50  
15 GCTGAATTAA GCAGAAAGGG CTTGAATCC TGGCCTAGAA TTTGGGCAGA 100  
TACAGCATT ACAAACCGC GCATCTC 127

## (2) INFORMATION FOR SEQ ID :737:

20

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 64 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :737:

GCCTGCGCCG ACCACCCCTT CCTTTTCTTC ATCCAGCACA GCAAGACCAA 50  
CAGGATTCTC TTCT 64

35

## (2) INFORMATION FOR SEQ ID :738:

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

372

(xi) SEQUENCE DESCRIPTION: SEQ ID :738:

5           GCCAGCGCCG ACAATGCCCC GAATCCAGAA CTTGCTAT CACTCTCCCC           50  
          AACAACCTAG ACGCGAAAAC AGAATAAACT TCACCCAG           88

(2) INFORMATION FOR SEQ ID :739:

10           (i) SEQUENCE CHARACTERISTICS:  
              (A) LENGTH: 95 base pairs  
              (B) TYPE: nucleic acid  
              (C) STRANDEDNESS: double  
              (D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :739:

20           GCCAGCGCCG AGATCCTGGC GGCCTACCGC CCCCCGTGCA CCCCCGCTAG           50  
          CGCCCCACCC CGCGTCTACC GCCCAATAAA GGCATCTTTG CCGGG           95

(2) INFORMATION FOR SEQ ID :740:

25

          (i) SEQUENCE CHARACTERISTICS:  
              (A) LENGTH: 245 base pairs  
              (B) TYPE: nucleic acid  
              (C) STRANDEDNESS: double  
              (D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :740:

35

          GCCACCCCGA AGACGTATCA AGGCCCTCGA ACAACCCCGA GAGCTGATGA           50  
          GATGAATGAG AAGATGCCGA ACTTTGCGCA CTCCATGCCC CTGCTGCAGA           100  
40           CAGTAACCAA GAGCAAGGAC CAGGGCACCC ATGAGGATTA TGTGCAAGGA           150  
          CTTCGGGTGT TTGACAAGGA AGGAAATGGC ACCGTCATGG GTGCTGAAAT           200

373

CCGGCATGTT CTTGTCACAC TGGGTGAGAA GATGACAGAG GAAGA

245

## (2) INFORMATION FOR SEQ ID :741:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :741:

15 GCCTGCGCCG ACGATGCCCCA GAATCCAGAA CTTGCTCTAT CACTCTCCCC 50

AACAACTAG ATGTGAAAAC AGAATAAACT TCACCCAG 88

## (2) INFORMATION FOR SEQ ID :742:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 242 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :742:

30

GCCGGAGCCA AAGCAAGCCA GAAGACTAAC AGTACTAACT ACAAATATTC 50

GCACCTCGAT CGCAGTACCC AGGTTCTCAC GTAGCTGAAG NAATGTATTA 100

35 CTCTGATAGT CTTCAATTCGG ATAGACTAAA GCGTGTGCTG ACTGGAGATG 150

AGGTAAAGAA GATATGTATG CAACGTCCAG TCAAAACGGA TGGCAAGGTT 200

CGAGTCATGT CATATACCTT GCTGGATTAA TGGATGTCAT TA 242

40

## (2) INFORMATION FOR SEQ ID :743:

374

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :743:

10

GCCTGCGCCG ACCACCCCTT CCTTTTCTTG ATCTAGCACA GCAAGACCAA

50

CGGGATTCTC TTCT

64

15

## (2) INFORMATION FOR SEQ ID :744:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :744:

GCCAGCGCCG AGGTTGTATA TTTCTAGGTG CAGGTATATG ATTGCCATAT

50

AATAAAAATT TGAAAACAT

69

30

## (2) INFORMATION FOR SEQ ID :745:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

35

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :745:

375

GCCAGCTCCG AGGTTGTATA TTTCCAGGTG CAGATATATG ATTGCCATAT 50

AATAAAAATC TGAAAACATC CCAC 74

5 (2) INFORMATION FOR SEQ ID :746:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :746:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTGTCTAT CACTCTCCCC 50

AACAACCTAG ATGTGAAAAC AGGATAAACT TCACCCAG 88

20

(2) INFORMATION FOR SEQ ID :747:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 base pairs

25 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :747:

GCCTGCGCCG ACGATGCCCA GAATCCAGAA CTTGTCTAT CACTCTCCCC 50

35 AACAACCTAG ATGTGAAAAC AGAATAAACT TCACCCAG 88

(2) INFORMATION FOR SEQ ID :748:

(i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 178 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

376

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :748:

GCCAGCACCG ATGAATTCCC TTGACCCAA GTCTGCAGCA GGTCCCTTTT 50  
GCGCTTCCTT CCCCTCAGGC AGCCTCTTTC CCCCTGGGCC ACTCCCGGGG 100  
10 GCGAGGGGGC TACCCCTTTC CCAGGCTTTT TATTCCCGTG GGGCTCACCC 150  
CAAAGCATTAA AAAGCAGCTT TGCAATTC 178

15 (2) INFORMATION FOR SEQ ID :749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 235 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :749:

GCCAGCACCG AAAAGCCAAG ACTTCATGAA CTACACAGGT CTTACCATTG 50  
ACCTAAGATC AATCTGAACT ATCTTAGCCC AGTCAGGGAG CTCTATTCCT 100  
30 AGAAAGGCAT CTTTCGCCAG TGGATTGCC CCAAGGTGA GGCCGCCATT 150  
GGAAGACGAA AAATTGCACT CCCTTGGCGC AGACAAACAC CAGTTCCCAT 200  
35 TGGCGCTGCT GCCTATAACA AACACTTTTT TTTT 235

(2) INFORMATION FOR SEQ ID :750:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

377

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :750:

GCCTACGCCG AAAACCCCTT CCTTTTTTTC ATCCAGAAAA GCAAGAGAAA 50

AAGGATTCTC TTCTGCGGCC GCCAACGCGT CGGAGAT 87

10

(2) INFORMATION FOR SEQ ID :751:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 170 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :751:

GCCTCCGCCG ATTCGTGACC AAGAAGGCTC TATGCATTCA GGCTTTCCAG 50

25

GAGACTCAAA AGCTGAAGAA GCAAAGAAGA GCCTTAAAGG CTGCAGCAGC 100

AGTCCNAAAA ACAAGCAGAG CAGAGGAACC CAGACAGCCC TGCCAAAGCC 150

ATGCCAAAGA CACTCAAAGA 170

30

(2) INFORMATION FOR SEQ ID :752:

(i) SEQUENCE CHARACTERISTICS:

35

(A) LENGTH: 72 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :752:

378

GCCAGCACCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT 50

AATAAAAAAA TGAAAACACC CC 72

5 (2) INFORMATION FOR SEQ ID :753:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 122 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :753:

GCCAGCGCCG AGGACACCAA GAAGGTTTG GACAGCGTGG GCATCGAGGC 50

20 GGACAACAAC CAGCTCAACA AGGCCATTAG TGAGCTGAAT GAAAAAACA 100

TTGAAGACGT TATTGNCCAG GA 122

(2) INFORMATION FOR SEQ ID :754:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH 243 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :754:

35 GCCACGCGCG ACTGAACTG CACCGACCCC CCCTCGAGGA CCTGCTCTTA 50

GGTTCAGAAG CAAACCTCAC GTGCACACTG ACCGACCTAA GAGACGCCTC 100

AGGCGCCACC TTCACCTGGA CACCCTCAAG CGGGAAGAGC ACTGTTCAAG 150

40 GACCACCTAA GCATGACCTC TACGGCTGCT ACAGCGTGTC CAGTGCCCTG 200



379

CCGGGCTGCG CCGAGCCATG GAACCATGGG AAGACCTTCA CTT

243

## (2) INFORMATION FOR SEQ ID :755:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :755:

15 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGCATATG ATTGCCATAT 50

AACAAAAACC TGAAAGCATC A 71

## (2) INFORMATION FOR SEQ ID :756:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 243 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :756:

30

GCCACCGCCG AGTGACGCCA AAGCCCTTGG TTGACTCTAA CAGCCCCGTG 50

GGCGCGCGGG AGGCCGGGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT 100

35 TAGTGCTTTT TCAGTGGGGC GGGCGGGGAA GCAGGCGGGA CCAGGCAGCC 150

AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA 200

GACGTCGCCA ACCAGAACTG ACGCGCGACC TCCTGGGCGC TGA 243

40

## (2) INFORMATION FOR SEQ ID :757:

380

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :757:

10

GCCTGCGCCG ACCACCCCTT CCTTTTTTTT ATCCAGCACA GCAAGACCAA 50

CAGGATTCTC TTCC 64

15

## (2) INFORMATION FOR SEQ ID :758:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 243 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

20

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :758:

GCCAGCACCA AGTGACGCCA AAGCCCCTAG TTGACTCTAA CAGCCCCGTG 50

GGCGCGCGGG AGGCCGAGCG CTCTAGGGTC TACCTATCAG CGCAATCGTT 100

30

TAGCGCTTTT TCAATGGGGC AGGGCAGGAA GCAGGCGGGA CCAGGCAGCC 150

AGTTCTCAAA GGCTGCGGGG CCGACTAGAG GCCACAGCCC CTCACCCCTA 200

35

GACGTCGACA ACCAGAACTG ACGTGCAGCC TCCCGGGCGC CGA 243

## (2) INFORMATION FOR SEQ ID :759:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

40

381

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :759:

GCCACACCAG ACTTTCGACC CCCCAACCCT CTGAGGAAGA TGGGGGCAAG 50  
AAGATCACGC TCCCCGCCTG TTCCCCCGCC GCTTTTCTCC TCTCTTCTCT 100  
10 CTTGCTCTC AGCTCCCCCT GTCCCCTCAG CTCCAGACGT AGGGGAGGGG 150  
TTGCCACAGA CTCCCTGCTT GAAGCCTGCC CTTGCCTAAG ATGCTGGTAA 200  
15 TGGCCATGGT ACCCCCTTCC GGGCATCTAC TCTGGTTTTC GGCCA 245

(2) INFORMATION FOR SEQ ID :760:

(i) SEQUENCE CHARACTERISTICS:  
20 (A) LENGTH: 68 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :760:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ACTGCCATAT 50  
30 AACAAAAACC NTGAAAAC 68

(2) INFORMATION FOR SEQ ID :761:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 71 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

382

## (xi) SEQUENCE DESCRIPTION: SEQ ID :761:

GCCAGCGCCG AGGTCGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50  
5 AATAAAAACT GAAACACCCC C 71

## (2) INFORMATION FOR SEQ ID :762:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :762:

GCCTGCGCCG ACGATGACCA GAATCCAGAA CTTTGCTTAT CACTCTCCCC 50  
20 AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

## (2) INFORMATION FOR SEQ ID :763:

## (i) SEQUENCE CHARACTERISTICS:

25 (A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :763:

35 GCCTGCGCCG ACAAACAAA CCTGGAGGCC ATTCTGCACA GCCTGCCCCGA 50  
GAACTGTGCC AGCTGGCGGT GAGGGCTGCC CAGATCCCCG GCACACACTC 100  
CCCCACCTGC TGTTTACATG ACCCAGGGGG CGCACACTAC CCCACAGGCG 150  
40 CGCCCATACA GACATTCCCC GGAGCCGGCT GCTGCGAACT CGACCCCGTG 200

383

CGGATAGTCA CACTCCCTGC CGA

223

## (2) INFORMATION FOR SEQ ID :764:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 70 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :764:

15 GCCAGCGCCG AGGTTGCATA TTTCTAGGCG CAGGTATATG ATTGCCATAT 50  
AATAAAAATC TGAAAACACC 70

## (2) INFORMATION FOR SEQ ID :765:

20

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 118 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :765:

30

GCCAGCGCCG ACCGCCCCAA AAATACTCCC ACCGGGATCA GGGCGATTAA 50  
TGAAGACTCA ACGGGGACTA AAAAGGGGCC CCAAAAAAAAA CCAACCACC 100  
35 TTTCTACGTA CCGTATAG 118

## (2) INFORMATION FOR SEQ ID :766:

- 40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 88 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

384

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :766:

GCCAGCGCCG ACGATGCCCA GAATCCAGGA CTTGCCTAT CACTCTCCCC 50

AACAACTAG ACGCGAAAAC AGAATAAACT TCACCCAG 88

10

(2) INFORMATION FOR SEQ ID :767:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 base pairs

15 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :767:

GCCACCGCCG ACTCCAGGCA CTCACTCAA CTTGATCTTC AACTCTGCAT 50

25 ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTTCAAT T 91

(2) INFORMATION FOR SEQ ID :768:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 223 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :768:

GCCTGCGCCG AACAAATATA CAGAATGCGC GAGTCCCTCT GGAAGCCCAA 50

40

CATGGATCCG GATCACCTGT TTGAAACCAT CTCCCAAGCC ATGCTGAATG 100

385

CTGCGGACCA GGATGCAGTG CCAGGCATGG GAGTCATTGC CCACATCACC 150

GAGAAGGACA AAATCACCAC CAGGACACTG AAGGCCCGAA TGGACTCGCC 200

5 CTGCTCCCAG AGCCCACTTT TTT 223

(2) INFORMATION FOR SEQ ID :769:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :769:

GCCAGCGCCG AAAACACACA CTTTGCTTCT TACCTGC 37

20

(2) INFORMATION FOR SEQ ID :770:

(i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 37 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :770:

GCCAGCGCCG AAAACACACA CTCTGCTTCT TACCTGC 37

35

(2) INFORMATION FOR SEQ ID :771:

(i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 91 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

386

## (xi) SEQUENCE DESCRIPTION: SEQ ID :771:

5 GCCACCGCCG ACTCCAGGCA CTCACTCAAA CTCGATCTTC AACTCTGCAT 50  
ACAAGCAGAA GCAATAAACC AATCTGATTT TCTTTTCAAT T 91

## (2) INFORMATION FOR SEQ ID :772:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :772:

20 GCCTGCGCCG ANGCAATCCC TTTGACCTGA GTCTGCAGCA GGTCCCTTTT 50  
GCGCTTCCTT CCCCTCAGGT AGCCTCTCTC CCCCTGGGCC ACTCCCGGGG 100  
GTGAGGGGGT TACCCCTTCC CAGTGTTTTT TATTTCCGTG GGGCTCACCC 150  
25 CAAAGTATTA AAAGCAACTT TGCAATT 177

## (2) INFORMATION FOR SEQ ID :773:

30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 151 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :773:

40 AACATAAGAG GAGAAAGGAA GGGACATGAG GCATACCATT CCCCCCCCCA 50



387

GAATTAGAGG TAAAGGAATC CTAATAATAA GAGCACAGCA GCAATCACAC 100

TCACAGGGTC CAGAGGCGTA TTCCTGGCCA TCTTCCTAGT ACTCGGTCCG 150

5 T 151

## (2) INFORMATION FOR SEQ ID :774:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 299 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID:774:

ATCTTAATGA ACATGGCATT TAAATCCTG TAATTTCAA CAGTGAACCA 50

20

CAATGCCGTA TGATCTAAG GCTGCTGAAC CACAGCGTGG ATACACTTAA 100

CTGAGCTCCT CGCTGGGTCA AAGCACTCAT CTCCGAGTCT AAAGCTACAC 150

25

ACTATGGAGC ACACAACTCT GCCTCGCGCT GACACCAGAC AAACACGGCG 200

GGAGCTGAGG CGGACAGCTA CAGGACCACG AGCATAGACC ACGGCACCTG 250

AGACCATCTC TACGCAAGGA CTTAAGGAAG CAAATATAAT ATTAAATA 299

30

## (2) INFORMATION FOR SEQ ID :775:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :775:

388

5 TGAAGGAAAT GACTACCTTG CACTACATGA AAAGGATATC GTTGCCATTG 50  
TGGCGTAATT TTCGTGCCGA GTGAATGTGG CGCAAACAAC TATATATCNA 100  
AACCGTATAT TTAAATGAA TTACTAGAGA GGAATGTAA TCATGGCAA 150  
AGAAATTAAG TTTTAAGAAG ATGCTAGTGC TAAGC 185

## (2) INFORMATION FOR SEQ ID :776:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :776:

20

ATCCAAGCCC ATACCCATCA ACAATGGGAC AGCGATTGGA TCACCAGCCA 50  
TTTCACCACA CATGGCAACA AACTTACCTT CTTTAAGAGC GGCAGTAATC 100  
25 ACATCGTCGA TCAAACGCAA AATCGATGGG TTATAAGGTC GATACAAATA 150  
AGCAACCTTA TCATTACCAC GATCTGCAGC CATCGTATAA CCAATCAAAT 200  
CGTCGGTACC AATCGAGAAG AAGTCCAATC CCTTAGCAAA CTCATCAGCC 250  
30 AACAT 255

## (2) INFORMATION FOR SEQ ID :777:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

389

## (xi) SEQUENCE DESCRIPTION: SEQ ID :777:

|    |  |     |
|----|--|-----|
|    | AGATTCTGCA GTGTAATATG ACCAAATCAA ATCCGTTGTA TGATCGAATA | 50  |
| 5  | AGGCCGTCAT AAAGTAAGTT GAAAATTCG TTCTGGCTG AATCGTCTTA   | 100 |
|    | AACCGTTGTA CACAACGTAG TAAATTCAT AACCCATCTG CATACCAATC  | 150 |
|    | GTCAGCCGTG ATGCATTTAC TCACTTTACG TCGATGAATG TCAAACATCG | 200 |
| 10 | CACCTTTTCA ATGTTTACTA AAAACATAGC ACGCAATAT             | 239 |

## (2) INFORMATION FOR SEQ ID :778:

|    |                               |
|----|-------------------------------|
| 15 | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 252 base pairs    |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |
|    | (D) TOPOLOGY: linear          |
| 20 |                               |

## (xi) SEQUENCE DESCRIPTION: SEQ ID :778:

|    |   |     |
|----|---|-----|
| 25 | ACTGAACAAC GTAAGGTCTT GACTGACACT TACAAGTTGG ATGAATCTGA  | 50  |
|    | AATAAAGTTG GTATTGTTTG AAGCAGCCCA ACAATTTCTGA ACATGCTACA | 100 |
|    | AGACCGTCGT TTGACTGACA AGGCCTTGAA GTACATGACT GACAACAACG  | 150 |
| 30 | TCGATCTTCG CCTAGGCGCC ATGGTCACTG GTGTTGACGA AAATGGCGTG  | 200 |
|    | ATTTTAAAGG ATGACTCAAC TTCGCCAACT CGGTTCTCTA TTAGGACAAC  | 250 |
| 35 | TA  | 252 |

## (2) INFORMATION FOR SEQ ID :779:

|    |                               |
|----|-------------------------------|
| 40 | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 265 base pairs    |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |

390

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :779:

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| TCGGATTTAT | ACGGCTGTTA | GTGCTATCGG | CGTCTGGTAT | GTGTTATATA | 50  |
| TCGCCTATCG | TTTTTTGGCC | AATGGGCGTT | GGCTACGCGG | GGCAATGATT | 100 |
| 10         | GCCATCGTTT | TTGTTATCTT | GACTTATTTT | GTCATTTTAA | 150 |
|            | ATATTATTTA |            |            |            |     |
|            | ACTATTTTAC | AAATAAAGTG | GTCAAATGGG | ATATTTTGCC | 200 |
|            | AAAAATAGAG |            |            |            |     |
| 15         | AAAGTGTTAG | GCGGCCCA   | GCTGGAGGAA | GAGAAAGCGG | 250 |
|            | CTGTGCATGA |            |            |            |     |
|            | AGTTATTGCA | CCCGC      |            |            | 265 |

20 (2) INFORMATION FOR SEQ ID :780:

|                               |
|-------------------------------|
| (i) SEQUENCE CHARACTERISTICS: |
| (A) LENGTH: 249 base pairs    |
| (B) TYPE: nucleic acid        |
| (C) STRANDEDNESS: double      |
| 25 (D) TOPOLOGY: linear       |

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :780:

|            |            |            |            |            |     |
|------------|------------|------------|------------|------------|-----|
| CTCAGCTGGA | CCAAATTAGT | TGAATTACTC | ACCATCAATA | AACTATAAAT | 50  |
| GGCGCCAATG | ACCAACCCGC | CAACGATTCC | CGTTGTCAAA | GAACCTAATA | 100 |
| 35         | ACAAGTAACC | AACCGCAGCC | CCAACAAGCC | CAACTAGGTT | 150 |
|            | TAAAAAACC  |            |            |            |     |
|            | AAGCAAAAGG | CCAACTGTCC | GTCGTTTATT | GGATTGTATC | 200 |
|            | TGCTCATATA |            |            |            |     |
|            | ACATTAAAC  | TTAACCGTTG | GCACTTCTTT | CTCAGACCCG | 249 |
| 40         | CCGATACTG  |            |            |            |     |

(2) INFORMATION FOR SEQ ID :781:

391

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :781:

10

GAGAGAACCC ACCATAGTAC TGTCTCCTGC AGACAAGACC AACGGCAAGG 50  
CCGCCTGGGG TAAGGTCGGC GCGCACCTGG CGAGTATGGT GCGGAGGCCC 100  
TGGAGAGGAT GTTCCTGTCC TTCCCCACCA CCANNNACTA CTTCCCGCAC 150  
TTCGACCTGA GCCACGGCTC TGCCAGGTT AAGGGCCA 188

15

## (2) INFORMATION FOR SEQ ID :782:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :782:

30

AATATTTATT TCATTTGTTT ACTACCACTT CATTTTATTT GTTGCTGCT 50  
GCCGTTTTAT TTATTTTAC TGAAAGTGAG AGGGAACCTT TGTGGCCTCC 100  
AACCTTTTTC TGTAGGCCGC CTTAAGCTTT CTAAATTTGG AACATCTAAC 150  
AAGCTGAAGN GGAAAAGGGG GTTTCGCAAA AT 182

35

## (2) INFORMATION FOR SEQ ID :783:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs

392

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :783:

|    |  |     |
|----|--|-----|
|    | CACAGCCAGA GCTTCGTCCT CAGTGACCAC AGGGCTGAGC CAGGCTCAAC | 50  |
| 10 | CGGCTTCTGG CTCTTGTTTT GCAGAAGAAG AACTAGAAGC AAGGNGCTTT | 100 |
|    | CCTCCGGGTC CCAGAGCTGT TAGTGATGGA GCCAGGCCTG GGATCCAGCT | 150 |
| 15 | TTCCTGAGTT CCTGACCCCT GCTATTTTAT TAGTCAGCTC TCAGCACTTA | 200 |
|    | CCAGAGGAAC AGGCAGCCTT TTGGCTACTG CCTTCAGAGA AAGAGAGATG | 250 |
|    | AGAGAATTCA AATGCGTGTT GGTGTTCTG TTAGTACAAG CAGCA       | 295 |

20

## (2) INFORMATION FOR SEQ ID :784:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :784:

|    |   |     |
|----|---|-----|
|    | CAATAGCGAC TTCTGGTGTC AATTCGATAA TCGGCCAATG GATACTTCAC  | 50  |
| 35 | GTGTGTTTCA TCGTCTGTAA TAACGGCGAA TGGTGTCAC T CAGAACCAG  | 100 |
|    | TACCTGATGT TGTGGAATG GCAACCATT T GTGTCAAACG CACTGGTAGA  | 150 |
|    | ACTTCACGAT ACGCTTACGG ATGTCCATGA ACTTTTGTT C TATTTCCATG | 200 |
| 40 | AACAATTCCT TGATACCTTC TTCGTCTGAC AAAATACCTT CGTGACGTGT  | 250 |

393

TGAGTATTTCG TACAAGAAGC GACCAATCTT ACCGGCATCA AGTGC

295

## (2) INFORMATION FOR SEQ ID :785:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 303 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :785:

15 GTGTAAAGCG AGTAGCCCCC AAATCAGTCA TCTTGGCCTG AAGATGTAAA 50  
CAAGGAGGTT TGCTTCCTGC AAGATGAGTA CTTCACTGAG TTTGGTTTTTC 100  
ATTTTTCCTA CACCGAAGCC ACCTCTGTCC ATCCAATGTT CATGTCTGTG 150  
20 CGAGGCTGCG CAGGAGGTTA CGTCAAGATG TGGCCAATAA AGTCCAAAAA 200  
GCGCTTTGAA TACTGTTCTG GGTTCACGGT GGAGATCTCC GCGCAGCCAT 250  
25 GTTTAACAGT TTTTGCAGCA TGGGCAGCTT TCTTTTTTGC ATCATAATGA 300  
GTA 303

## (2) INFORMATION FOR SEQ ID :786:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :786:

40

TATGGCGCGG ATCCTAACGG CTGGAATGAA GATATGCCAA CGTACAGCCT

50

394

CTATGACCCA GCCATGGGAT CAGGCTCATT GCTTTTGACG ACTGCTTCAT 100  
ACATGAAGAA TGATGGTGTT CGTGGGGCCA TTAAGTACTA AGCCAAGAAG 150  
5 TTATCACGAC AACCTATAAC TTGGGCCGAA TTAAGTTGAT GATGCACGGG 200  
GTGGAGTATA ACGATATCAA TATCCATAAT GCAGATACCT TGAGTTCAGA 250  
CTGGC 255

10

(2) INFORMATION FOR SEQ ID :787:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 206 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :787:

CATTGAAAAG TGCCTGAAAA ATGGTAAATT CTAAATGTG TGTGAGATTG 50  
25 TCAGAATCAA CAAAACTAGG TTGGTTAAAC ATATCTCTGG TACATCAAGG 100  
GGCATGATAC AAACCAGTCT AAAGACTGTT TATAAAGGAG AGAGCTGGCG 150  
ACTTATTTTT ATTTTTTTTT TTTGGACAG ACTCCCTTTG TCCCCAGGCC 200  
30 GGAGTG 206

(2) INFORMATION FOR SEQ ID :788:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40



395

## (xi) SEQUENCE DESCRIPTION: SEQ ID :788:

|    |  |     |
|----|--|-----|
|    | ACAAATAGCG ACCTCCTGGA GAAAAATCGA AAACGGCCAA GTGGATACCT | 50  |
| 5  | CACGTGGTTC ACGTCTGAAC AACGGCGAAT GTGAGCTACC TCAGAACCAG | 100 |
|    | TACCCGAAGT TGCTGGAAGG CAACCACATT TGGTCAAAC GAGGCGTGGA  | 150 |
|    | AGAACCTCAC GACACGCTTA CGGAGTCCAT GAACGCTTGT TGCAATCCAG | 200 |
| 10 | GAACAATTCC GCGACACCCT TCGTCTGACA AAAAACCTTC GTGACGCGTC | 250 |
|    | GAGTATCCGC   | 260 |

## 15 (2) INFORMATION FOR SEQ ID :789:

## (i) SEQUENCE CHARACTERISTICS:

|    |                            |
|----|----------------------------|
|    | (A) LENGTH: 208 base pairs |
|    | (B) TYPE: nucleic acid     |
| 20 | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :789:

|    |  |     |
|----|--|-----|
|    | AACCCACCAT GGTGCTGTCT CCTGCCGACA AGACCAACGT CAAGGCCGCC | 50  |
|    | TGGGGTAAGG TCGGCCTGCG CACTATGCGT GAGTATGATG CAGAGGCCCT | 100 |
| 30 | GGAGAGGATG TTCCTGTCCT TCCCCACCAC CAAGCCCTAC TTCCGCACT  | 150 |
|    | TCGACCTGAG CCACGGCTCT GCCGAGGTTA GGGGCCACGA CAAGAAGTG  | 200 |
| 35 | ATCGACGC   | 208 |

## (2) INFORMATION FOR SEQ ID :790:

## (i) SEQUENCE CHARACTERISTICS:

|    |                            |
|----|----------------------------|
| 40 | (A) LENGTH: 289 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |

396

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :790:

AAAAGAAGTA CGGTAAGGCA AATCCTGAAA TTAAGAGTTA CTATGTGCCT 50  
GAAAATACAT TGTTCTACTC ATTTAGTGTG ATGGCAATGG GCGCCGGCGC 100  
10 ACTCTTGCTA TCGACCATCG TCGCGCTTGG GATGAACCGT CGTAAGTCAC 150  
AATTAATGTA GACACAACGT CGATTCTCGT GACTTATGGG GATCGCAACT 200  
15 TTCGCGCCAT TCTCGATCAA CACAGCCGGT TGGTCAGTGA CTGAATTAGG 250  
TCGTTATCCA TGGGTTGTTT ATGGCTTGAT GCTAATAGC 289

20 (2) INFORMATION FOR SEQ ID :791:

(1) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
25 (D) TOPOLOGY: linear

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :791:

TTTCCTGTGG AAGTAGTTAA ATTGATAAAT TCCAAAAATT TGGCAATTAA 50  
TTGCTCATT TTAATGGTAG AGTTTCCATT AATGAAGTTG GAAAATACGG 100  
35 TGAATCTTTC AATGAACTCA GTTAGACATT CGGAATGAGC TTCATACATT 150  
GTCTTATTAT CTTTCTTCAA TTTATCCTCC AAATCTGGGA ATTCTGATAA 200  
CCAAATTGAA GCACCTTATC TATGATCCGG GC 232

40

(2) INFORMATION FOR SEQ ID :792:

397

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :792:

10

TTTCAACAAA CAGAAACCAA TTTCCAACCA GAGGGCGATT TCTCCTTGTC 50

TGGTAATATC GAACAAACTA TTTTAAAGAA CTTGATTCTT GGCAACATTA 100

15

AGAGCGCTGT GAAAAATTCT CTAGAGAATG ACTTACTAAC GGAGGCCATG 150

GCGATCGCAT TAGATTCAAA TAACGAAAGA TCAAAGGAAA GTGTCAAGAA 200

TGCCTATTTC GCGAAGTATG GATCTAAATA AC 232

20

## (2) INFORMATION FOR SEQ ID :793:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :793:

GGGAACATAT CTTACGGTA GTGANCCAG TGACCAGATG TCTTATACAA 50

35

GTTCAAGTTA GACAAAACGG GTGTATACAC GTGTTGGTAA CCATTGGCCA 100

ATTCTTTGTC GGTGATGTAA CGTTCAACTT GACGGCGAAG CGATTGCCCC 150

ATTTGGTAAC CAAACTGGCA AACCTGAACC CACTTCTTGA CTCGTAAAGA 200

40

ACAAGTCCAT GTCACGACCA ATCGTCCGGT GGTCACGTTC TTAGCTTCT 250

398

TCACGACGTG CAATTCTGCT TCAACGTCGG CTGCTTCCA TT

292

## (2) INFORMATION FOR SEQ ID :794:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 288 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :794:

15 CAGCAGGCAC AACACCATCG GTTGTGCTG AAAGTATTTT TAAGTCTTTG 50  
GCCAAGAAGT CAGTTTCAGC TAAGTTAGAC GGCACCTATG CGGGTATGCA 100  
TGATGTCATT CCTGCATCCG ATGATTTTTA ATTAATTACA ACAACTGATG 150  
20 ATGAAGCGTC GAATTCGTCG CGTCATTCTG CCTCACACTC ACAGGCACAA 200  
GCCTTAAAGC ATTTGCCAAA GTTTGCTAAC ATGCACTTTG GCGCGGCAAC 250  
25 CATTTATTGA AAATGGTTTC TACTATGATA CAAATAAC 288

## (2) INFORMATION FOR SEQ ID :795:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 258 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :795:

GTGGCTATGT ATAAGCAGAT ATTATCTAGT AAATGTAAAG TGAACCCAAT 50  
40 CGATAGACCC AAAAAGTGTT TTAAGTGGAA AACACCTTAT GAGGTTTATT 100

399

TTGATGAAGT GTTGCAGTTG GTTTGATAAT TCAAGGCATT AAGGCAATAT 150  
CTCAATCACC GCATTTTCCA CAACCGGCCA CAAAACAGCT CGTCTATTTC 200  
5 GAGGTCAGTT ACGGCGTCCA GTCTTTGAGC AGATGATTG CCCCAGTGA 250  
TCGTCGGC 258

(2) INFORMATION FOR SEQ ID :796:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :796:

20

TGCTTCAAAG CCTGGCTTAA CCGGCTTGCC CACCAACTTC AATTATACCT 50  
GCCOCTTTGC CTAACATCTC ACCGACTCGG GCAACCATCG TATCAACACC 100  
25 CGCGACTCGA TCCCCATCGT AAAATGATTC CGAACTAACA TTTAACACAC 150  
AATAGATAAT ACCATCAGCA TAATGCAAGG TTTTACCATC CACGACCCAG 200  
AGGCGATCAA TCGCGACTAA CCGTCGTTGT AATTCAGGAC TAGCGGTACG 250  
30 CTCATGTAAC GCGACAATAT 270

(2) INFORMATION FOR SEQ ID :797:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

400

## (xi) SEQUENCE DESCRIPTION: SEQ ID :797:

5      AAATATCGCT GCGTGCAGCT GAGTTACTAG CTGTTGAAAC TTATCGTTAC      50  
10      TTGTGTAGGT TGTCTGAAAC GGTCCGAGTC ACCGGTTAGC TTGATAAGTC      100  
15      AGGTTTTTCAG CAACTGTCAT CAAGCCATCA CGACCTATAT AAGCCACTGC      150  
20      AATCGCACTT TACATCATTAG AGACCCTTAC TAGAAGTAAC TGGCCATCCT      200  
25      GCCACCGCTT      210

## (2) INFORMATION FOR SEQ ID :798:

30      (i) SEQUENCE CHARACTERISTICS:  
35          (A) LENGTH: 218 base pairs  
40          (B) TYPE: nucleic acid  
45          (C) STRANDEDNESS: double  
50          (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :798:

55      ATCATAAGCG CTGGAAGTTG GGGCATTGTA CAGGGACAAC TTCGGCCTTT      50  
60      GTTAGCCCCA AGAGTCTACA CTCTGCCAAT GGTGCGCTCC ATAGGAAAAA      100  
65      CCACGGTCCA AGGCAGAAAC TACGAACCTC AGATAACCGC AAAGAGGATA      150  
70      TCAACCAGAG GACCGAAATG TAAGCCTATT TTAGCCCAAA TAACGAGACA      200  
75      AGTAGTTGAG CTAAATGC      218

## (2) INFORMATION FOR SEQ ID :799:

80      (i) SEQUENCE CHARACTERISTICS:  
85          (A) LENGTH: 176 base pairs  
90          (B) TYPE: nucleic acid  
95          (C) STRANDEDNESS: double  
100          (D) TOPOLOGY: linear

401

## (xi) SEQUENCE DESCRIPTION: SEQ ID :799:

|    |  |     |
|----|--|-----|
| 5  | CCTATCAGAA TCCAATGAGA ACTACAATGG TGTGCCCAGA CGTAGAGCTG | 50  |
|    | AGAATAGCAT TACCAAATGG AACAACTGTC TACAGTCAGG ATTAAAAAGA | 100 |
|    | ACAATACTAC AAACCAAGTA TATCAGGCTA TTATAGCAA GGCTGCCATG  | 150 |
| 10 | AACAATACAA CACTGAATTA CTCGGC                           | 176 |

## (2) INFORMATION FOR SEQ ID :800:

## (i) SEQUENCE CHARACTERISTICS:

|    |                            |
|----|----------------------------|
| 15 | (A) LENGTH: 254 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :800:

|    |  |     |
|----|--|-----|
| 25 | GCAATTGCTT AATTGTCT TCCTTCTTAG CATTTTGCTG AGAAGCCAAA   | 50  |
|    | CGTTGCGCCA ATTCAGAAGA TTCACGCCAG AAGTCGTAGT TACCAACGAA | 100 |
|    | TGGTGTGATC TTACCAAAGT CAACATCCAA GATGTTGGTT GACACGGCGT | 150 |
| 30 | TTAGGAAGTG ACGGTCGTGG GATACCACAA TCACTAGGTT CGGGAAATCA | 200 |
|    | GCCAAGAAAT CTTCTAACCA GTTAATTGTC TGCACATCCA GACCGTTGGT | 250 |
| 35 | TCGA   | 254 |

## (2) INFORMATION FOR SEQ ID :801:

## (i) SEQUENCE CHARACTERISTICS:

|    |                            |
|----|----------------------------|
| 40 | (A) LENGTH: 203 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

402

## (xi) SEQUENCE DESCRIPTION: SEQ ID :801:

5 ATCCAGGCCC ATACCCATCA ACCCTGAAAC AACGATTGAA TCACCAGCCA 50  
TTTAACCACA CATTGCAACA AACTCACATT GGGTTCCGAG CGGCAGTAAT 100  
AACACAGTCG ATCAAACGCA AAATAGATGG GCAATAAGGT CGATACAAAT 150  
10 AGGCAACCTT ACAATTACCA CGATCTGTAG CTATCGTATA ACCAATGAAA 200  
ATG 203

## 15 (2) INFORMATION FOR SEQ ID :802:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :802:

GACACAACCTG TGTTCACCTAG CAACCTCAAA CAGACACCAT GGTGCACCTG 50  
ACTCCTGAGG AGAAGTCTGC CGTTACTGCC CTGTGGGCTA GGCGAACGTG 100  
30 GATGAAGTCG ATGGCGAGGC CCTGGGCAGG CTGCTGGCGA TCTACCCTTG 150  
GACCCAGAGG TTCTTTGAGT CCTTTGAGGA TCTGTCAACT TCC 193

## 35 (2) INFORMATION FOR SEQ ID :803:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



403

## (xi) SEQUENCE DESCRIPTION: SEQ ID :803:

5 AACAAAAGTT GAAAATTTTA AATGGTCTTT TTATGGTTTG CGTGACCTAA 50  
AAAGACAAAG TTTATCCTTG CCTTACTGTA TAGAAATGCG TCGTATCCAC 100  
AATAGCGTAC AGATTTTTCG GCATTAATCC GTGTTTATAT TAACAGATTC 150  
10 GTTAAGTATC GTTTAAAAAG GGAGAGAGGG GATACCCTCT CTCTAGATAA 200  
ATGGGTCATC ATTTAATCCC AAGAATGATG TCGATAAGTA CTTTCTAAA 250  
CGATAACAAG AACCCAGTA GGTAGTATAG CAGTCTTAA 290  
15

## (2) INFORMATION FOR SEQ ID :804:

## (i) SEQUENCE CHARACTERISTICS:

20 (A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :804:

AACTTGATGG TCGAGGCCAT CTCCTGGGCC GCCTGACGAT ACCGTGGCTA 50  
30 AACAGGTACT GCTGGGCCGG AAGGTGGTGG TCGTACGCTG TGAAGGCATC 100  
AACATTTCCG GCAATTTCTA CAGAAACAAG TTGAAGTACC TGACTTTCCT 150  
CCGCAAGCGA ATGAACACCA ACCCTTCCCG AGGCCCCTAC CACTTCCGGG 200  
35 CCCCAGCCG CATATTCCGG CGGACCGTGC GAGGTATGCT GTCCCACAAA 250  
ACAGGG 256

## 40 (2) INFORMATION FOR SEQ ID :805:

## (i) SEQUENCE CHARACTERISTICS:

404

- (A) LENGTH: 286 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :805:

|    |                                      |     |
|----|--------------------------------------|-----|
| 10 | AGCAACCTCA AACAGACACC ATGGCGCACC TGA | 50  |
|    | CTCCTGA GGAGAAGTCT                   |     |
|    | GCCGTTACTG CCCCTGTGGG ACCAGACGAA     | 100 |
|    | CGCGGATGAA GTCGGCGGCG                |     |
|    | AGGCCCTGGG CAGGCTGCTG ACCGATTAC      | 150 |
| 15 | CCTTGGACCC AGAGATTCTT                |     |
|    | TGAGTCCTTT GAGAATCTGT CCACTTCTGA     | 200 |
|    | TGCTGTTATG GGCAACCCTA                |     |
|    | AGACGAAGGC TCATGGCAAG AAGTGTTCG      | 250 |
|    | GTGCCTTTAG TGATGACCTG                |     |
| 20 | GCTCACCTGG ACGACCTCAA GGGCACCTTT     | 286 |
|    | GCACAC                               |     |

## (2) INFORMATION FOR SEQ ID :806:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 291 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :806:

|    |                                  |     |
|----|----------------------------------|-----|
| 35 | TTCTTCATCA GATTTTACAT CTGCCTGATT | 50  |
|    | AGAATCTTCT ACACTGGCCT            |     |
|    | CAGAAGATGA TTGTTCAAAA CTTTTCTAA  | 100 |
|    | GTTGCTGTAA AAAA                  |     |
|    | AACTTCC                          |     |
|    | ACGGACAAAG TAAAATGCAG TTCTTTATCG | 150 |
|    | TTAGCCAGT GTACAACAA              |     |
| 40 | AGGTCCAATC TTCTCTTCAT TTAATTCAG  | 200 |
|    | ACTCAGAGAT GTAATAGATG            |     |
|    | GAAGAAGTGA AATGTCTGTG GCTGGGTGA  | 250 |
|    | TGCTGGCTGC AATATGAAAG            |     |

405

TGGCAAAGTG CATTGCTATG CAGTGGAGTG TTACTGTGGA C

291

## (2) INFORMATION FOR SEQ ID :807:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 276 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :807:

|    |   |     |
|----|---|-----|
| 15 | AGTTTAATCA GCTGCAATGA AAACAAACGT CTTTATTAG GCAGAATCCA   | 50  |
|    | GATGCTCAAG GCCCTTCATA ATATCCCTTA ATTTAGTAGT CGAACTTAGG  | 100 |
|    | GAACAAAGGA ACCTTTAACA GAAATAGAAC AACAAAGAAAG CGAACTTAGC | 150 |
| 20 | GATACTCGCG GGCCAGGGCA TTAGCCACAC CAACCACCAC TTTACGATAG  | 200 |
|    | GCAACCTGCA CTGGAGGGGC GACTTCTCCG CCAAAGCGAC GGGCCAGCAC  | 250 |
| 25 | ACAGACCAGC ACGTCGCCCCA GGAGCC                           | 276 |

## (2) INFORMATION FOR SEQ ID :808:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :808:

|    |  |     |
|----|--|-----|
| 40 | GGCCTGCCAA CAGCATAGGG AAGAATCTCA TTGTTATACA TATTAAGAAT | 50  |
|    | CGATTCTAAA TAGACCTTTT TACCAGTCGC TGAAACTCTT AAATTAAGTA | 100 |

406

ACATCGCTAG CTAATTTTCG TAATGGCCGA TTAATCTTGA AACGGCGGCG 150  
AAGCTTGTTTTC TTCACACGTT TCCCTTCAGG TCCTTTGATG AATCATACTG 200  
5 ACGTGATCGC TTATCGTA 218

## (2) INFORMATION FOR SEQ ID :809:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 276 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear
- 15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :809:

AGCAACCCAG CGCTCAATGG TGCTAGTGAA CACAGTTGTG TCAGAAACAA 50  
20 CCTCAAACAG ACACCATGGT GCACCTGACT CCTGAGGAGA AGTCTGCCGT 100  
TACTGCCCTG TGGGCAAAGG CGAACGCGGA TGAAGTCGGC GGCGAGGCCC 150  
25 TGGGCAGGCT GCTGGCGATC TACCCTCGGA CCCAGAGGTT CTTTGAGTCC 200  
TTTGGGGATC TGTCCATTAC TGATGCCGTA TGGGCAACCC TAAGGCGAAG 250  
ACTAATGGCA AGCAAGTGCT AGACGC 276

30

## (2) INFORMATION FOR SEQ ID :810:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 199 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :810:

407

50  
100  
5 150  
199

GACTCCACCT GAACGGGCCC CTTCTGAACC GCCTCTGTGG GAGCAGGCCC  
CATCTGAGGA GGGTCCATCT GAGCAGATCC CTTCTCAACA GGTTCCTTCT  
GAGGAGGCTT ACTGCTTTTC TTA CTCTGATT TATTTTTCAG AGTTTCTTC  
TTCGTACTTT TTTTAACGCA AGTATTTTGC TTTTATTCT CCTCCATT

## (2) INFORMATION FOR SEQ ID :811:

10

## (i) SEQUENCE CHARACTERISTICS:

- 15 (A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :811:

20

50  
100  
25 150  
200  
250  
30 254

AAACAGCACA ACCAATGACA GGATGCAAGA ACTGATAGGG CGCCGCAAAA  
AAAAAGCGGG CCAAAGATGA AGTAAATAAA CGTAAGGGAG GTACCGAATC  
TGGGGGGCTT GGCCTAGAGT AAGGGAGAGG AGCTTCAACT ATCTCAATAA  
GGGCAAGAAA ACACAAACAA CTCCTTCATT CGTCCAAAAT GCTTCTGAAT  
TGCACCACAA TTGACACACA CACACCTCAA AGCAGAATCC GCACTGACCT  
AAGT

## (2) INFORMATION FOR SEQ ID :812:

35

## (i) SEQUENCE CHARACTERISTICS:

- 40 (A) LENGTH: 284 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

408

## (xi) SEQUENCE DESCRIPTION: SEQ ID :812:

TTTTTTTTTT AGCAATGAAA ATAAAAGTTT TTTATCAGGC AGACTCCAGA 50  
5 CGCTCAAGGC CTTTCACAAC ACCCCCCAAT TTAGCAATAG ACTTCAGGGA 100  
CCAAAGGACC CTTTAACAGA AATAGAACAA CAAGAAAACA AACTCAAAGA 150  
CACTCGAGGG CCAGGGCCTC ACCACACCAA CCCCCACTTC CAAACAGGCA 200  
10 ACCTGCACCG GAGGGGAGAC TTTTCGCCA AAGCGACGGG CCAGCACACA 250  
GACCAACACA TCGCCCAGGA ACCTGAAGTT TTCA 284

## 15 (2) INFORMATION FOR SEQ ID :813:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :813:

ATACAACAGC AGAAACAGGT ATCCACGCAC AGTCCAGCAA CATTTCTTCT 50  
GGTACAACGC AGCTTCAAAG TTCACATCAA ACGTTACTTT GTCATACCAA 100  
30 GGCAAGGATG CTAACTCGAA GTCAATCACG CGAGTGATGT CATTACAAC 150  
CGGTCACGGT GCCGATGTGA CAATCAAGAC TGAAGGCGAT GACGAAGAAG 200  
35 CAGCACTGCC CGCCGATAAC CGCAGCGATG CAAAAAAAAG AGCTAGACGA 250  
CTGACGAAAC CTGAGAACCC CGAAGGACT 279

## (2) INFORMATION FOR SEQ ID :814:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs

409

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :814:

|    |  |     |
|----|--|-----|
| 10 | AACGTGCTGG TCTGTGTGCT GGCCCATCAC TTTGGCAAAG AATTCACCCC | 50  |
|    | ACCAGTGCAG GCTGCCTATC AGAAAGTGGC GGCTGGCGTG GCAACAGTGA | 100 |
|    | CTGAGAAGAC CAAAGAGCAA GTGACAAACG CCGAAGGAGC AGTGGCGACG | 150 |
| 15 | GGCGTGACAG CAGTAGCCCA GAAGACAGCG GAGGGAGCAG GGGGCATCGC | 200 |
|    | AGCAGCCA   | 208 |

20

## (2) INFORMATION FOR SEQ ID :815:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 25 (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :815:

|    |  |     |
|----|--|-----|
| 30 | AAACCACGCT CAGTCAGGTT CCGGCAGCAG CTGCAGCATC TCATCTTCTG | 50  |
|    | CGACTCTCGG TGCCCTCTCC TTCCGATTTC CGGAAACATG GCCTCCGATG | 100 |
| 35 | TGGCTGTCTC TGACGACGTC ATCAAGGTGT TCAACGACAT GAAGGCGCAC | 150 |
|    | AAGTCTTCAA CGCCAGAGGA GGTGAAGAGG CGCAAGCAGA TA         | 192 |

40

## (2) INFORMATION FOR SEQ ID :816:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 bas pairs

410

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :816:

GAGAGAACCC ACCATGGAGC TGTCTCCTGC CGACAAGACC AACGTCAAGG 50  
10 CCGCCTGGGG TAAGGTAGGC GCGCACAATG GCGAGTATGG TCGCAGAGGC 100  
CCTGGAAAGG ATGCTCCTGT CCTTCCCCAC CATGTGAGAC CTACTCCACA 150  
15 CACTTCGACC TGAGCCACGC CTCTGCCAGG TTAAGGGCCA CGGCAAGAAG 200  
GTGCCCCGACG CGCTGACCAA CGCCGTGCGC ACGTGGACGA CATGCCCAAC 250  
GCGCTGTCCC CCTG 264

20

## (2) INFORMATION FOR SEQ ID :817:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :817:

ACCCTACACA CATCCGTTCA ACTGTCCCAT CACCCACTTA CACTCCAAAA 50  
35 AAAACCACTC AACAAAGCAA CAACCCATCC TGTTTTCATA ACGTTATCGT 100  
AAC AAAG CCGACCATAA TCAACTGAA TTTACTTCAC CACAAGGCAA 150  
AGCGATTATT TAGATGAGGC ACTCGCACTA CTGCTTGAAG TGCTACTAGA 200  
40 TG 202



411

## (2) INFORMATION FOR SEQ ID :818:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 179 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :818:

AGTAGAAAAT AAGTTCAAAA TTTAGAAAT ACTGGCTTTA TACTCGCCCA 50  
TGTATTTACA TTCACAGAGA TCTTTATTTA TTTACAAGCG CTTTGAGTTA 100  
CTGTATAGTT TTTTAAACA AAAAAGCGTG GGGGGCTCCC TTTAGCATTG 150  
CCCATAGGAT AGGTAATGAA CTTTTTGT 179

20

## (2) INFORMATION FOR SEQ ID :819:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :819:

TGTGCTCTTA TGCTAGATTT ACGGACAGAT TTTCTTCTGC CCTGTAACT 50  
AATAGCATAG GAGCATTTTT TAATACGATT CGATACAAA AAGAATTTAA 100  
GCAATCTCTC GCCGAGACGC ACAATCAAGA CCATTCATAT ACTGATCTAT 150  
CCGCTGAATA CGAACCTTCA ATCGACTCAA TCCGTAAGTG GATCAAGTTG 200  
TACGCGGGTC CACGAAGTGA CAGACGAAA ATGAACGCAA GCTGATGTAA 250

40

412

ACGCATCACA

260

## (2) INFORMATION FOR SEQ ID :820:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 226 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :820:

15 ACTCGGCACT TTCTTAGAAT AGACAATTG CAAAATGTCC ATCCCAGGTT 50  
CATCCTTGTA GCCTAATGTT TCCGTCACCG TTGCCACTAG TTAACGTGGG 100  
TGAACCTTAT CTGGGAAACG GGTAACATCC GCGACCACAA CTAGACCATC 150  
20 ATTTGACGTA ATGCCATCAG CACTCACCAA AACTTGGCCA ACCAACAGCC 200  
TTCCGTAAC TGAGTTTGAT TTCTCC 226

## 25 (2) INFORMATION FOR SEQ ID :821:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :821:

CACCTACATA TAGATGCACG AAGTACTTGC TCACCTTTTT TGGTTGTAAA 50  
TTTTCAAAGC GTTGAAGGCA GCATTCTTAG CGGCACGGAT GTCCTTATCA 100  
40 GTGAATGAAT CAGGCTTTTC CATGGCCAAC CAACCAACGA TTCGCATCGC 150

413

GTGATTTCGA ATCATGTCAA GCAAAGCACC GGCTGTATCA TAGTAAC

197

(2) INFORMATION FOR SEQ ID :822:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 304 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :822:

15 GGACTGGGTG CAGTGGCTCA CACCTCACGT TACATTTTAT AGCTAGCAGG 50  
GTAATGGGGA GTTATGGCAC TCAGGTCACA TTCTAGGGAA TGTTTATCGG 100  
GCAATCTCAA TGGCACCGCA AGCTAAATGA CTTCCAGTGT TTCTCATCTT 150  
20 TGGCCTTTCT TCATCGCAAC CTTTGCCCAA GACATCTGTT TTTTCTGGAT 200  
CACCCCTTGCA CAGCCACTGA GGAATGATCT TCTGAAAGTG AATCTTCAGT 250  
25 AGACACATCG CCACACCATC TANGTCAGCC ATCACATGCC CAGGTCTNGA 300  
CATG 304

(2) INFORMATION FOR SEQ ID :823:

30

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :823:

40

GGCCCAGCAG ANGGAGGAAC ACTACCGAGG CTCCAGCTTA ACGGTATTTG

50

414

GAGGTCAGCA CGGTGCTCAC AGAAGCCAGG AACTTGCCCA GGGAGGCGTG 100  
CACCAANGGG GCGAACTCNC GGGGAGGCGG GCGACCAGGG TCACCAGCAG 150  
5 GCAGTGCTTA GGAGCTGGGA GCCGACCAG CCCACCGAAC TCGCGCG 197

## (2) INFORMATION FOR SEQ ID :824:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :824:

20 AAAACAATG TCATTTTGTA CAGACAAAT TTAGCAGACT CAAGCTTCCA 50  
CAGTTAGTGC GAGAGCCTGT GGATGGCATA GTTACATAAG AGTCTGTTGT 100  
GGATTCAAAT GTCACCTCTT CCAGGCAGTC TTTCCTGACT TACCCTGGCA 150  
25 GCTTTGTGTT CCCACATTAC TAGTAATGTT TTTTTCCTTA ATAGCAATGA 200  
TTTCACTGTA ATAATGTATT TATATGCCTC TCTCCCCCAG ACAGCAAGCG 250  
30 TTTTCCCACA GGTCTCGACA CACAGAAGAT A 281

## (2) INFORMATION FOR SEQ ID :825:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 312 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :825:

415

TATTAAATTT ACTAGAATGT TACAGTTACA AATTGGTAA TGTTCCTTCT 50  
GAAAAACAGC CTAATTTTGC AGCCTGAAAC TTGACTGAAA ATCTCAATAC 100  
5 TTTTATTCAT GATAGAAAAA TAATTCCTGG CTTCATCTCA CAATTAACTA 150  
ATAATTATGT TAATATAAAA TATAACTGTG CCCTTCTTT TCAGTGATGA 200  
TCAAAGTGAT TCTCCCAGGC CAAAAATCA AATAAGAAGT TATATTTTAA 250  
10 AAAGACATAA CAAGCCATTC TACCCAGTGG GCATCTTCAG TGTACTCCCT 300  
CTACTAATTG GC 312

15 (2) INFORMATION FOR SEQ ID :826:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 189 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :826:

ACACCAAACA CGGGGAGTGG GGAGTAGAGG CTCTGGAGGT CAGGATGGCA 50  
GGGCAGGGAG GGGGAAGGAAG GAGTTGTTGG TCTCACAGTG TGCCTGCCAA 100  
30 TCCCAAAGCC CTAGAGACCC CTTCACTGCA GCACCTGCCC CCGGGTCTCA 150  
GGCAGCTTCA GGGCCAGAGA GCTGCCAAGG GCAAGCAAA 189

35 (2) INFORMATION FOR SEQ ID :827:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 232 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

416

## (xi) SEQUENCE DESCRIPTION: SEQ ID :827:

5 CTCTTAAGGG CTTGAAAATT TCTGTGGGAG TAGGACAGAG TGTAGAACGT 50  
ACAGTAAAAG GCAATAAAAC AGTGGGAATA ATTTTACCAG CTATGAGTAA 100  
AGGAGTAATG GGTATTTACT GCCTGTCATT AATCCACACA TATATCCATT 150  
10 TTAGAGATTA TTTTGTGCCC TGGAAATCTG TCTCATCACA GAGTGTTAAT 200  
ATACACCGGC GGGATATCA AGAGTGGCTA AG 232

## (2) INFORMATION FOR SEQ ID :828:

15

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 282 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :828:

25

GGACATTGGA AACTATACT CTATTATTGC GGTGCGTCCT AGCAGTCTCG 50  
CGCATGTCTC CTCAGCGCGC ACAGTCTCTC TCAGAGAGCT CTTCTCTCTT 100  
30 TATATGCGCA GACCCGCAGA CTGGGAGACC CAGACCCAGG GCAAACCTCTC 150  
TTCTTAGGTA TATCGCACCC ATCATATCTC ACACATCGTG TATGTCGTAT 200  
CATCAGACCC CCATAGAGCA TATATGCTAA ATTAATGCTC TCTTTCATCA 250  
35 GTAATTACCC CATATCATAA AATGCGGGCG GG 282

## (2) INFORMATION FOR SEQ ID :829:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 230 base pairs  
(B) TYPE: nucleic acid

417

(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :829:

|    |  |     |
|----|--|-----|
|    | CACTACATCC GCAAGTACAA CCGCTTCGAG AAGCGCCACA AGAACATGTC | 50  |
| 10 | TGTACACCTG TCCCCCTGCT TCAGGGACGT CCAGATCGGT GACATCGTCA | 100 |
|    | AGTGGGCGAG TGCCAACCTC TGAGCAAGAC AGTGCCTTC AACGTGCTCA  | 150 |
|    | AGGTCACCAA GGCTGCCGGC ACCAAGAAGC AGTTCAGAA GTTCTGAGGC  | 200 |
| 15 | TGGACATCGG CCCGCTCCCC ACAATGAAAT                       | 230 |

(2) INFORMATION FOR SEQ ID :830:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 226 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :830:

|    |  |     |
|----|--|-----|
| 30 | TTCCGCAAAT AAAAGAATTC ACTAAGGTAC CAAAACAGAA AATATACAGA | 50  |
|    | GATCAATGAC TTTCATATAC ATTAACAAAC AAAAGTTCAG AGATAAATG  | 100 |
|    | GAAGAGAAAT GCTGTTTTTA ACAGTATAAT TAAGATAAAA TATGAAGGTA | 150 |
| 35 | TAAACTTAAC AAGAAATGTT GCAAAACCAT TATGTGAAAA TTACAACACT | 200 |
|    | CCTGAAGACG CAGACACACC TAACAA                           | 226 |

40

(2) INFORMATION FOR SEQ ID :831:

(i) SEQUENCE CHARACTERISTICS:

418

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :831:

|    |  |     |
|----|--|-----|
| 10 | AGAAGTCCTT CCAAGAGTCT TGGGTATGCA ACAGCCATGG AGGCTGTGAC | 50  |
|    | CTTTTCCTT CTTTCTIACA GCCTGCAGTT CATTTAAGGA TCACCGGAGA  | 100 |
|    | TGACTCGTGC TCTAGTTCTT AAAATCAAAC AAGGATCTGC CAAATCCAAG | 150 |
| 15 | ACCCTGAATT TGGCCCAAAT TTGTAGAAAC ATTGCTTTTT ACCACCCGGT | 200 |
|    | GCACCAAAAA TACCTCCCAT TTCAAGGCAA CAACCGCTT AATTGCT     | 247 |

## 20 (2) INFORMATION FOR SEQ ID :832:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 base pairs
- (B) TYPE: nucleic acid
- 25 (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID :832:

|    |  |     |
|----|--|-----|
|    | CACCAGGCAG GGGATCCCGG AGGGAAGCCC TCTGCCAGGG ACATGGTGAG | 50  |
|    | GGCGTGGCCA TCACCCACGA AGGGAGCATA AATAACACTG GCAGGTGGGT | 100 |
| 35 | GGGCAGCAGG AG  | 112 |

## (2) INFORMATION FOR SEQ ID :833:

## 40 (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid



419

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :833:

AGCCATTCCC ACTAGAGGCC AAACCGCCTG CCCACAGAGA TTGACAGCCA 50

10 ATGTTTCATCT CATAACTCTC CTCCCAGCAG TGCACCAGTA AACTCAGATG 100

CCTGAGTGCT TGTGGCCACC ACACAACAGA TCGGCCTTC CTCTTCACTG 150

GCCCCTCGGC TGCTGCTGGG TCC 173

15

(2) INFORMATION FOR SEQ ID :834:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 base pairs

20 (B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :834:

TGGCCCATGG GAGCCCTTAT GAGCAAGTTT CCAGGTCCTT ATGACACAAT 50

30 TCCATCATTG TTCGGGTACA TCCTTACTCT CTGGCACAGT AGAGATGTTT 100

CAGACTTATC TTATATTTTC ACTTCCCAT ACCTGGAATC AATCACTTCT 150

CCGAGGATGC TTGATTCCTT TTAGTGAAGA ACAGTCTTTG GAAACCAACC 200

35

GTCTAGGGAC ATCAAGTATG TTTGCCGCTA TTGGAGTGTC ATTGCTCCTG 250

AACCTTCTAA GTGGACACAG CTAGGAAATG TATGTGCT 288

40

(2) INFORMATION FOR SEQ ID :835:

(i) SEQUENCE CHARACTERISTICS:

420

- (A) LENGTH: 310 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :835:

|    |  |     |
|----|--|-----|
| 10 | CTTTTCTATT TTCCTTAAGT GTCTGCCAGT CTGAGAAATA AAGGGACAGA | 50  |
|    | GTACAAAAGA GAGAAATTTT AAAGCTGGGT GTCCGGGGGA GACATCACAT | 100 |
|    | GTCGGCAGGT TCCGTGATGC CCCACAAGCC ACAAACCAG CAAGTTTTTA  | 150 |
| 15 | TTAGTGATT TAAAAGGGGA GGGAGTGAC GAATAGGGTG CGGGTCACAG   | 200 |
|    | AGATAACGTG CTTACAAGA TAATAGAATA TCACAAGGCA AATGGAGGCA  | 250 |
| 20 | GAACGAGATC ACAGGACCAC AGAACTGGGA CCAAATAAAG ATTGCTAAGA | 300 |
|    | ACGTCTAGGG   | 310 |

## (2) INFORMATION FOR SEQ ID :836:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :836:

35

|    |  |     |
|----|--|-----|
|    | TCAGTGGAGG AATTAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT  | 50  |
|    | GAAATGCCAA GGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA | 100 |
| 40 | GAGGTAATCA AAAACTTGAG CATGTATTTA AGGATCCATG ATTGAATTA  | 150 |
|    | CATCTCCCAA AATGCCTAGC ATTCTTC                          | 177 |

421

## (2) INFORMATION FOR SEQ ID :837:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :837:

CCGTTGCACT TGGTGTGGC ATTCTGCAGG GCGGCACTCT CCCACTCTTC 50  
15 CCGGCCTCGA GCCAACCTGA CGGCAGCCAG ATGGCAGTCG TAGTGACAA 100  
TGTGAAGTG GGACACGGTG CTGTAGCCCT GCTGT 135

## (2) INFORMATION FOR SEQ ID :838:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 201 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :838:

30

TCAGTGGAGG AATTAAACT GGTGGAGAAG GGGAGGTCAG GTTATCAGTT 50  
GAAATGCCAA CGTTATCTCT AATCTTAGCT AGATTCTGCC AAAGTTCACA 100  
35 GAGGTAATCA AAAACTCGAG CATGTATTTC AGGATCCATG ATTGAATTGA 150  
CATCTCCCAA AACGCCTAGC ATTCTTCGCC ACATTACAGT AGCAACATCA 200  
G 201

40

## (2) INFORMATION FOR SEQ ID :839:

422

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 181 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

5 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :839:

10 TTCTTTGGAG TACATCCTTA CTTTCTGCAC AACAGATGAG AGATGTTCCA 50  
GAACTTATAC TGTATCATAT ATTTTACCTC CCCCCCTATA CACCCTGAGA 100  
15 TATACATATA CACTATCTCC GCTAGAGAGA TGTCTATGAC ATATCACTTT 150  
CTGAGATGTA CACGAACGAG ATCTTTTGAG A 181

## (2) INFORMATION FOR SEQ ID :840:

20

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

25 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :840:

30 CATACAAATG ATTAGAAAGC AATACAGCCT TATTGCTGAT ATGGAGAAGG 50  
TTTTAGTGAA CATTGAGAGG AGTTTGAAG AAAGTCGCTG CACAATCTTC 100  
35 ATGGATGACT TTGAGGGATT CAAGACTTCA GTGGAAGAAC TAACTGCATA 150  
TGTGAGTAGA AATGCCAGGA GAACTAGAGT TCGAAGTAGG AGCTGGAAGA 200  
TAATAACATG GGTTTAAAAA AC 222

40

## (2) INFORMATION FOR SEQ ID :841:

423

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :841:

10

CGCTCAGCTG GTCTATCCTG CTCTTCCTCT TGTCTTGCT CTTGCTGGG 50

CTCCTATCTA CCGGCTACCT GCTGCCCCTG TTGCTCCTGC TACCGGCTCC 100

15

GACTCTGGCG GAGGCTCTTC TCCTGGCTCC TGCCCCCTGCT CACAACTCCC 150

TCGCTTCTCC TCCTCCACTC TCCTCTCCCG ACTCCTGCTC CGACTTTTGC 200

TCTTACTTTT ATGCCTGCTA GGACTCCGGC TCTTGGGTTT CCCGAACATT 250

20

GTCATTGTTT TGGAATTCT CTTCAGCTT GGTCTTTTGC CGG 293

## (2) INFORMATION FOR SEQ ID :842:

25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 239 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :842:

35 ATGAGGAGGT GAGGAAAAGG AGAAGTGCAG CTACCATCGA GTGATTCTTC 50

TGGGATAGGT GTCTCATTTA AATCTCATAA TCATCTTTT TGGCAGGTCA 100

GTCAACTTCA GGCTCACAGA TGACAGACAG TTGGCCCCAA GACACACAGG 150

40

AAATACATAA GTGACAACGG AATACAAGTC CATGAATTAA AAAACCATGC 200

424

TTTTCTCTCC TTGCCACACA GCTTTAGTTT GAAAAAAA

239

## (2) INFORMATION FOR SEQ ID :843:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 154 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :843:

15 TTCCGAATTA TTGAATCTTC TTCTGTAACA TCACAATCTT CCTGGTTTTTC 50  
AGAATAAACG CTCTTCTCGC TCGCCTCTCT CTGCACTCAC TCCCACCTCA 100  
CTCACTCACT CTATAATAAA ATGTTTGACAC TCAATTTATA TAGTAGTGTT 150  
20 TGTC 154

## (2) INFORMATION FOR SEQ ID :844:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 392 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :844:

35 GTCTTTAATT GAGAAAGCTG GAGTGGAGAC CCGATCCCCT GGGAGCAGTG 50  
CCAGGACTTG GGTGGAGACT GAGTGGGGTT TGTGTGGGTG AGGGGGCATC 100  
TACTCCTCTT GCAACAAGCC AGAAGTAGAA CAGCCTAAGG AAAAGTGACC 150  
40 TGCCTTGAG CTTAGTCCC TCCCTTAGGG CCCCCTCAGC CTACCCTATC 200

425

CAAGTCTGAG GCTATGGAAG TCTCCCTCCT AGTTCCTAG CAGGTTCCCC 250  
ATCTTTTCCA GGCTGCCCCT AGCACTCCAC GTTTTCTGA AAAAATCTAG 300  
5 ACAGGCCCTT TTTGGGTACC TAAAACCCAG CTGAGGTGT GAGCTGTAAG 350  
GTAAAGCAAG TTCTATCCAA TTAGAAGCTG TTGGGGGCGT AT 392

## (2) INFORMATION FOR SEQ ID :845:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :845:

20

CAAAGAATAA ATAATTTTTC TATTCCTGAA AGTTAACTAA TTATTTATTA 50  
GAAAGTCAGA AATATGTGGA AAGCAAAGGA ATATTGAGA AAGTGATATG 100  
25 AAATTAATAA GTGGTAAAAA ATTAATAAAA TTAATATTAG AGTTTCCTTT 150  
GAGCTAATCC TTTATTTATT TATTTTTTTC CTTGAGACAA TGTCTTGCCA 200

## (2) INFORMATION FOR SEQ ID :846:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :846:

40

TTAAAAATAC TCTGGAAGA GCACTTCCAT CGTTCATTTA CATCATATTA 50

.426

|    |  |     |
|----|--|-----|
|    | GAAATGGATT TCCGAGTCAG CACTGGCTTC CTCCAGAATA GCAGTCCTGG | 100 |
|    | AGGAGCGAGA TCTCCCCAAG CCTCCAGGAT TGCAGTCTGT TTGTGCCTT  | 150 |
| 5  | CACTCCCTAA TAGGTTTGCC TTATTAAAG GACCCACCTT CAGAGCTGCC  | 200 |
|    | AAGGACTTTC TCAGAGCAGC TCCTTGGTCC CTCCGACAGC CTGGGATGGC | 250 |
|    | ATTTATTCTG GGGCCTGGGT GTGGGGAGGT CCTCACCAGC CTAGGAGTAA | 300 |
| 10 | GAGGAGGTGG T   | 311 |

(2) INFORMATION FOR SEQ ID :847:

|    |                               |
|----|-------------------------------|
| 15 | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 287 base pairs    |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |
|    | (D) TOPOLOGY: linear          |

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :847:

|    |  |     |
|----|--|-----|
| 25 | CAGATCAAGA CTGGTGCCCC TTGCCGATCT GAGCGCTTGG CCAAGTACAA | 50  |
|    | CTCAGCTCCT CAGAATTGAA GAGGAGCTGG GCAGCAAGGC TAAGTTTGCC | 100 |
|    | GGCAGGAACT TCAGAAACCC CTTGGCCGGG TAAGCTGTGG GCAGGCAAGC | 150 |
| 30 | CCTTCGGTCA CCTGTTGGCT ACACAGACCC CTCCCCTCGT GTCAGCTCAG | 200 |
|    | GCAGCTCGAG GCCCCGACC AACACTTGCA GGGGTCCCTG CTAGTTAGCG  | 250 |
| 35 | CCCCACCGCC GTGGAGTTCG TACCGCTTCC TTAGTCT               | 287 |

(2) INFORMATION FOR SEQ ID :848:

|    |                               |
|----|-------------------------------|
| 40 | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 263 base pairs    |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |



427

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :848:

|    |  |     |
|----|--|-----|
|    | GATTACAGGT GTGAGCCACC GTGCCTGGCC TATTAATATG CTCTTAAAC  | 50  |
|    | TCATCCATAC GTTTTCATAG CAAGAAAGCT TATTTCTCCC AACTACCGAA | 100 |
| 10 | TAATATTCTA TCGTATGGCC GCACCTCTGT TTATCCATT ACCTATCGAG  | 150 |
|    | AGGCATCTTG ATTACTTCTA GCTTTGGATT ATTACAAATA AAATATAACA | 200 |
| 15 | AACACGCAAA CAGAGTTTCT CGTGTGAATA TAAACCCGCA AACCGGCTGG | 250 |
|    | AGGCATATNA CCA   | 263 |

20 (2) INFORMATION FOR SEQ ID :849:

|    |                               |
|----|-------------------------------|
|    | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 279 base pairs    |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |
| 25 | (D) TOPOLOGY: linear          |

30 (xi) SEQUENCE DESCRIPTION: SEQ ID :849:

|    |  |     |
|----|--|-----|
|    | TTGTCAGTCA GAATAGGATG TAAAGACTA TTTCAAAGAG TTAAATTATT  | 50  |
|    | TGTTAATATC AGAGATCAGC CACAGACAAG AAGTTTATGG ATGAGTGCAG | 100 |
| 35 | CAGTGGTCCA TTGGACATGT TAAATACTCG TGGATATCCA CAATTCGAAT | 150 |
|    | TGACATTAAA AACGAATGGA TACCCAACTC TGAATCCAT ATCGTTTTTT  | 200 |
|    | AATATCAAAA ACACAATTTT AACTACTGAT AAACCAGGCA ACCACCGCAA | 250 |
| 40 | GTTTATCGAA ATCCTGCCGC TACTAAACA                        | 279 |

428

## (2) INFORMATION FOR SEQ ID :850:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :850:

GCTGAAAGTT GAAGTGGAGA GCTTGAAACG AGAACTCCAG GACAAGAAAC 50  
AGCATCTGGA TAAACATGG GCTGATGTGG AGAATCTAAA CAGTCAGAAT 100  
GAAGCTGAGC TCCGACGCCA GTTCGAGGAG CGACAGCAGG AGACGGAGCA 150  
TGTTTATGAG CTCTCGACAG AAT 173

20

## (2) INFORMATION FOR SEQ ID :851:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :851:

TCGAGAAAGT TTCAATGTGA TTAGATTAAA ATTAAAAGAA TCCATAAAAA 50  
TGGAAACAAAG AAGAAGAGGA ATGAAATTAC TTTTACTTTA AACAGCATTG 100  
TTATCACATA AAACACGTAT CTTACAAATT CATGGGATAG CCCATAAATG 150  
GGACTACAGC AACAAATGGTA GGAGAGTCCA TCCTTCTTCA AAAGCAACCC 200  
AGCAGGAATT TTCTGTAAAA AATATTTTTC CCGTAATACT 240

40

429

## (2) INFORMATION FOR SEQ ID :852:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 314 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :852:

ACTGGACTGG TCAACAACAA AGCTCATGGC AATAGTCTTT TGGAAATGTTA 50  
15 AAGGAATTTT TCTAGTTGGC TTTCTGGAGG GCCAAAGAAC AACAAACATCT 100  
GCTTATTATG AAAGTGTTTT GAGAAAGCCA AAGCTTTAGC AGAAAAACAC 150  
CTGGGAAAGC TTCATTAGAG AGTCCTTCCC CATCACAACG CTTCTGCTTA 200  
20 TTCCTCTTAT AAAACAAGGG CAATTTGTG AGAGCTACTG ACGATTTTCC 250  
CCTCGAAATT TACTATTTCT ACAGCTTATT AATCTCAAAT AGTAAGCATG 300  
25 TCCTTGCCGT CACT 314

## (2) INFORMATION FOR SEQ ID :853:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 267 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :853:

TCCTGAAATA CTCTCTACTG TCACTGCTTC AGTTTAATTT ATAGATAGCA 50  
40 CCAGATATGA GTCCTTATTA GTTCTGATAA CTCTGAAATG GTTATTTGGT 100

430

ATTTCCTCAG TGACAAGCAA ACTATCCCCC CACATGCCTT TAATGGCCAG 150  
TGTTTTTCGAT TTGTATACCA ATAAGCAATC TAGGTAGAGG TAATCATATA 200  
5 CTGATACGCT AACCTTTGAA ACATAATTTC CAATCTAGTA AGCTAAAATC 250  
GCGCCAATAC TGCTTAA 267

(2) INFORMATION FOR SEQ ID :854:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :854:

20

GCAGTGGATC TTTCTTTTTT TCCAAAGGAA ATTTTCATATA GAGTCCATTC 50  
ATAGGAAACA GATAAAATGT GAACGGCTGC AACTGAGATG GGGGAGAGTG 100  
25 GCTTGGAGCC CCCAGCCTCT TTGCTTTCTC TTATCCCTAT AGGATGGCCA 150  
TTAGGTGAAG CAGTTTAGCT TGTGGTTCA GACCTG 186

(2) INFORMATION FOR SEQ ID :855:

30

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 162 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :855:

40

ATTTTGAAAA GAAACCTACA AAAATTGTAT TTCCATATT CATAGTCAGC 50

431

CAAAATATT GGTCAACTCA TGCTCTCTGC AAGGTTCTGC AAAAATTGCG 100

GAGTGGTATA GACAAGGCAC CATTGCAATA TATAATACTT TTTGGGTATT 150

5 GGCCCAAAAA TT 162

(2) INFORMATION FOR SEQ ID :856:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 286 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

(xi) SEQUENCE DESCRIPTION: SEQ ID :856:

TCTGTGGCCA CAGATGCATA TTACAAGCCC ATCCAGAGCC ATTATGAAGA 50

20 GAAAGTGGCA ATTTTATTCT CAGCCTGAGA AATCCACACC AATCTAGTCT 100

GGGTTTCCAA GGATCTGCCG TTTAAGTCAC TTAGCCTCTA TCCTTTCCGG 150

25 GAACAACCTG CCCCTAGAGA GGGTGAACGA GAATCGTCCC CAGTGCCTCC 200

AACATAACAA ACCCAATCGC CCTGTAACT TAAATCTTC AACTCGAGAA 250

30 AAAGGCTCAT GACTACTTCT AACCATGCCC AAACCC 286

(2) INFORMATION FOR SEQ ID :857:

(i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 280 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :857:

432

AACTATATGG TATTATTTCA CGCTGTACCC AGTCCATTGC TTGAACTTAC 50  
GGGTACCTAA TGAAACGTGG AGGTCCGGAT GTATGAAAAT CTCCTCTTTT 100  
5 CCCCTTTACT TACAGCCTCT GTAGGCAATA ATTATAGAGT AGTATAGATG 150  
ATTTTCTTT TTTATAAATC TGCCTATCTC CAGGAGGATG GGGCGCGCAC 200  
TTTTAGAAAT GCATATAAAT GCTCTACGCT CCTTTTTTCT GTTACTTAAT 250  
10 CGGCGCCAAG GCCTTTACAT GAATACTCAG 280

(2) INFORMATION FOR SEQ ID :858:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 310 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :858:

25 CACTGGTTTT CATGACTGAT TTCTTTATTT TTAGTAGTTC TGACATGTTG 50  
GCCAGGCTGG TCTTGAATC CCAGCCAACC TCAAAGTGCT GGGATTACAG 100  
CTGTGAGCAC CAGCCCAACC TCGCCTCTTT AAAAAGAAAA AACACAAGTC 150  
30 CACTCTGAAG TCAGCCTCTG TAACCTCCCC ACAAGAAAAC CGTTTTACAT 200  
CAGTCACTAA CCAAACAACC AACAGTGCTT CAACACAGAA AGTAAAGCAT 250  
35 TATACAGGGC TTGAACTGTC TTTTAAGCAA GCCCCAAATC CTTTGAAAGG 300  
AGGCAGTAAC 310

(2) INFORMATION FOR SEQ ID :859:

40

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 158 base pairs

433

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :859:

|    |  |     |
|----|--|-----|
| 10 | TCTGTGTGGA GGGGAGGGAC CCAGTCTGGA CCCAGGTGTC ATCATCTCAG | 50  |
|    | CCACAGCAGG GCCCTCTCAG GCTGGGAAAC TTCTGCCAGA GCTGGCGAGT | 100 |
|    | CCTCTGCAGG TCAAGCCAGG GCTTGGACAC AACTACTTCA TCTATCGCGC | 150 |
| 15 | AGGAAGAG   | 158 |

## (2) INFORMATION FOR SEQ ID :860:

## (i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
| 20 | (A) LENGTH: 263 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :860:

|    |  |     |
|----|--|-----|
| 30 | TTTCTAATAA GAACATAAAA TAAAGGCTAA TTAAAAGAAG GTGACTGAGT | 50  |
|    | CCAGGAAGGC ACTAATCAAA GATGATATAC AGCCAGGTAA AAAAGAACAA | 100 |
|    | TTCACAGGCA CAAGACTATA TAACCATCGT TTTATTTTCA AACGTTATAC | 150 |
| 35 | AAAATATACT CTACCGAACT ATAATAGATC ATTAATAGTG GCACAATCTT | 200 |
|    | TAGATTCGGA ATAACTTGAA AATAAATCCC AACCACGTAA CTTACTAAAG | 250 |
| 40 | GAATAATGAG CCA   | 263 |

## (2) INFORMATION FOR SEQ ID :861:

434

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 254 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :861:

10 ATTTGTCTGA AAAATATATT TCTACACGAT CTGATAAAGT TCAGATAAGG 50  
GGCATTCTAT TCCTAAGAAT GTCCTAAAAA TGGAAACTG ATAAAAGATT 100  
15 ATGCTTAGAA TTATACAGGT AAAAGACCTA CAACAATTGT TCTCTGTTT 150  
TGATCCCATG GGTCAATTGT TATTACTCTT CTTCAACAGA GTGATTTTCT 200  
ATTATAAACT TTCTTAGGAG CCAATACAGA GTAGAAAGAA ATATTTTCAG 250  
20 AAAG 254

## (2) INFORMATION FOR SEQ ID :862:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 300 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :862:

35 GTTCCTCCTT TGTAATTAT GAAATATTTA TAGTTTAGAC TGAGTAATAT 50  
GACATGAAAC AACAAACCTG CACATTTCTA ATTTATAACA AATCCGTTTC 100  
CTTAATGGGT GGAAGGAAAT CTGAGGACAA TTCTAAGGAG TCTTGCTGCG 150  
40 TTTCAGTGCG ATCTTCTAGT CATACTGAAG ACAATACCTC TCCAGATTGA 200



435

TCTTTCCCCT TCTTATACTC TTCCCGATCA ACGTCAATCA CACGCACCAC 250

TCCAGGTTTT AGACTTAGGT CATCCGTCTC TACCTGACTT CTGTTGCCCT 300

5 TCACCTACAC GTGGCTCGCT TTAGTTTGCT GAGCAGC 337

## (2) INFORMATION FOR SEQ ID :863:

## (i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 169 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :863:

TGGTGGGTTC GAGCCCAACT TCAGCGCTCT TCGAGAAGTG CGAGGCGAAC 50

20

GGTGCAGGGG CGCCTCTCCT CTCCACCTTC CTGCGGGAGG CCCTGCAAGC 100

TCTCAGCGAC GACGCCACCA TCTTCTGACC AACTTCAGGC TACTACCCCA 150

25

ACTTACAATG CCACCGCGA 169

## (2) INFORMATION FOR SEQ ID :864:

## (i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 286 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :864:

ATTAAGGTAA AGGAAGACTT TCCATTGTTA AGTAGAAAGA GTGTCCTGCT 50

40

ATTACTACCA TTCACATCTA GTTTGTGTGA ACTAGGGTTT TCTATCTTAA 100

436

CCCTGTAA AACAAGGAA AGAAATGGGC TGAATGGCGC ACCAGCTATG 150  
CGGATAGCAT TATCTTCCTG TGTTCCAGAC TGAATGAAT TTATGAACAA 200  
5 GGCAAGCACA CCATTATAGT AAATAAAATC TTACCTAGTT TTCGTTTTTG 250  
CATTTCTTAC TTCGCAGTAT TTCTCCCGCC AAGAGC 286

(2) INFORMATION FOR SEQ ID :865:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 272 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :865:

20

ATATAGTCCG CTAGGGATAG TGAAAAATTT GGGGCTTGGT TTAGATTGGA 50  
GAGGTATATG GTGGGGTGTC TTATAAGGCT TAACTTTGGG AGGGCCCAGG 100  
25 GCCTTGATTT CTGTCCCCCT TGCCTTGCCT GGCCTTTGAA TTGAAAGCTT 150  
TGAATTAGGC CTTCATAGAT TTTAGTGTGC ATACAAATAA CACGATCTTT 200  
TTATAAGGCA GATTATGATT CTGAAGGTTT AGTGTGGGAC CCAAGCTTTC 250  
30 GCATTTCTGA TCTATAAGGT GA 272

(2) INFORMATION FOR SEQ ID :866:

35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 40 (D) TOPOLOGY: linear

437

## (xi) SEQUENCE DESCRIPTION: SEQ ID :866:

ATGCAGGAGA AGAAGGATGC CAAACTAAGT CAAAAAAGC GAACGCAAAT 50  
5 AAAAGGAATG AGCACGGTTA CAAAGTCACA GGATGAGTCC CTGGGATCTG 100  
GGGCGGGAGA AGGGGTGAAT CAAGAATGAC TTGAGCTTGT TACTCCCTAG 150  
CAGGCTGAGG GCGTGACACA GCAGCTCGAT GACAAAGAGG TCTATTATAG 200  
10 TTTCTAACAC TACAACGCTA ACTTTTGGA CGTATCTACT TCTAGCATGT 250  
AGACAGATCT CTAATCGCCT GCCAGACGGT AAGCCGCAGG AATGCG 296

## 15 (2) INFORMATION FOR SEQ ID :867:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 25 (xi) SEQUENCE DESCRIPTION: SEQ ID :867:

TATTTTATCT CAACATAATA AAAACGACTA TAAATCTTCC TAAGAGAATG 50  
CTCTACTCCC AAGACTAATT TAAACTCGGG GATCGTCAGA GGGAGTGCCA 100  
30 CTGTGACTTC TACGATGAAA GAACAAGGGA GAGAAGATCT TATCGACAAT 150  
CATACAAAGC CATATATACG CTATTCCTCA ACTCACAGAG TTAATTAAAT 200  
35 GTCACCAGGA TGGAAGAAAC CTTATAAGCC CCTATCTATC A 241

## (2) INFORMATION FOR SEQ ID :868:

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 130 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double

438

(D) TOPOLOGY: linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID :868:

GGACGACTGC AAGCTGGAAC TACACACGCG CACTCGCTCA CACTACACAC 50  
ACGCCACTCT CACACACTCT CACACACGCA CCCTCTCGCG CATGCTCTCT 100  
CAAAGCCCAA TATAACCAAG GGAAGGAAT 130

(2) INFORMATION FOR SEQ ID :869:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 310 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :869:

25 TTCAATATT TATGTATGTT TGAACATTTT CATAATAAAA TGTGAAAAA 50  
CTAATGAGAA TGGCATAAAC AACATTTAAG CAATATATTT TGAATTAA 100  
TTCAATGGT CAAATTCCTG GAAACACAA ACTCCCTTCA CTAACAGAAT 150  
30 TGATAGAAAA TCTGAGTAGT TCACCATTGT TAAAGAAATG GAATGTGCCA 200  
TTTAAAACCC TCCAATTGAA AATACTACAT ATAGTTACAA TAGGGAATTT 250  
35 TCCAAGCAC TTAACAATA AACAATGCCC TCTTTATACA AACCTTCCC 300  
AGTAATAGAA 310

(2) INFORMATION FOR SEQ ID :870:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 192 base pairs

439

(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :870:

|    |  |     |
|----|--|-----|
| 10 | AAAGAGGCAA GTTCCTGGTG CAAAGGTGGC TCTGCAGCAT AATTTAGGCA | 50  |
|    | TTGGAGGAGC TGTGTGTTGT AACACTCTAC AAGATGGGTT TTCCGGAAGC | 100 |
|    | CGCCAGTTCT TTTAGAACTC ATCAAATTGA AGCTGTTCCA ACCAGCTCTG | 150 |
| 15 | CAAGTGATGG ATTTAAGGCA AATCTTGTTT TTAAGGAGAT TG         | 192 |

## (2) INFORMATION FOR SEQ ID :871:

## (i) SEQUENCE CHARACTERISTICS:

|    |                            |
|----|----------------------------|
| 20 | (A) LENGTH: 250 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :871:

|    |   |     |
|----|---|-----|
| 30 | ACCATAGATG TGTTCAGAG GCAAAGAGA CACATTATCC TAGATGGCAG    | 50  |
|    | AACATGCTTT CAAAACATAT AAAACGTCAA AGTTCAGAT CTTTCTACAT   | 100 |
|    | TTTAAATCCT GTCTGAGGAT GGCAGCTGAC TTTATGTAGC TGATAGACGA  | 150 |
| 35 | CTAGAGTTTC ATCCAAATAC CTGACCACGA CTTTCATGGAG ATTTGAATAA | 200 |
|    | TCTATCCGAT GAGATTTATA TNTAAACAAC TCAACTCCTG TCGAAACAAA  | 250 |

## (2) INFORMATION FOR SEQ ID :872:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 313 base pairs

440

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :872:

|    |  |     |
|----|--|-----|
| 10 | TCAGCTACGA ATTGCTTCCT TCTCACAGAA CTGTGACATT TATCCAGGGA | 50  |
|    | AGGATTTTGT ACAACCACCT ACCAAGATTG GCGTGGGCTG CCCCAGAGAT | 100 |
|    | ATACCCACCA ACAGCCCAGA GCTGGAGGAG ACACTGACTC ACACCATCAC | 150 |
| 15 | AAAGCTTAAT GCAGAGAATA ACGCAACTTT CTATTTCAAG ATTGACAATG | 200 |
|    | TGAAAAAAGC AAGAGTACAG GTGGTGGCTG GCAAGAAATA TTTTATTGAC | 250 |
|    | TTCGTGGCCA GGGAAACACA TGTTCCAAGG AAAGTAATGA AGAGTTGACC | 300 |
| 20 | GAAAGCTGTG AGA   | 313 |

## (2) INFORMATION FOR SEQ ID :873:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 270 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :873:

|    |  |     |
|----|--|-----|
| 35 | TAGATGCTGA TGGCAATGAC ACAATTGACT TCCCTGAATT CCTGACAATG | 50  |
|    | ATGGTAAGAA AAATGAAAGA CACAGACAAT GAAGAAGAAA TTAGAGAAGC | 100 |
|    | ATTCCGTGCG TTCGATAAGG ATGACAATGA CTATATTAAC GCTGCAGAAC | 150 |
| 40 | TTAACCATAC AATGACAAAC CCCGAAGAGA AGTTAATAAA TGAAGAAGTT | 200 |

441

GATGAAATGA TCAAAAACGT AGATNATTGA TGACGATGGT AAGGTAACT 250

ATCCAGCGTT AGCACAAATG 270

5 (2) INFORMATION FOR SEQ ID :874:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 229 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :874:

TTGGGCCATG TCCCCATTTT ATCTCCAAAG CCAGCCATGG TGTATTTCTC 50

TCTGCTTTTC TTCCATATTT CCAACCCAGA AATGACTCCT GTTCCCATAT 100

20 GTGATTATTA TATTGCGCTA ACCCAAGTGA TTAAGGATAA TCTCACTACT 150

TAATGACAGC TGATTATTTT CATCTGCAAA CTTACTCAAG AATGCAATCC 200

25 AGACTAACAC GACAATAGGA CATCAAGCT 229

(2) INFORMATION FOR SEQ ID :875:

(i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 294 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :875:

TTTGAACTTT CAGCCGAATA CATCTTTTTC CAAAGGAGTG AATTCAGGCC 50

40 CTTGTATCAC TGGCAGCAGG ACGTGACCAT GGAGAAGCTG TTGTGTTTCT 100

442

TGGTCTTGAC CAGCCTCTCT CATGCTTTTG GCCAGACAGA CATGTCGAGG 150  
AAGGCTTTTG TGTTCCTCAA AGAGTCGGAT ACTTCCTATG TATCCCTCAA 200  
5 AGCACCCTTA ACGAAGCCTC TCAAAGCCTT CACTGTGTGC CTCCACTTCT 250  
ACACGGAAC GTCTTCGACC CGTGGGTAAC AGTATTTTCT GCGT 294

## (2) INFORMATION FOR SEQ ID :876:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :876:

20

ATTTTGGTA ACATACATCA AGTGGCACTA ATTACACAGT AACTATAAGG 50  
TAACTAACAT GAAACCACAG AACTGTAACT CTGCCACAGC TGCATGAACT 100  
25 CGGGTTGTCC TGACCGAGCC CATCCCCAAA AAACCGCCCA CCCCAGAGCT 150  
ACGCCAACAA AAACCGTTAT TAA 173

## (2) INFORMATION FOR SEQ ID :877:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :877:

40

TAATCAAAAG AGCTCTAAAT CTGTAATTC TTTCTCCTTT AAAAAAATGT 50



443

CTACTTTGTT TTGGTCCTAG GCATTAGGTA ATATAACTGA TAATATACTG 100

AAACATATAA CGGAAGATGC AGATGATAAA ACTAATTTTCG AAC 143

5 (2) INFORMATION FOR SEQ ID :878:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :878:

ACTGAATAAA CTGCTGATGT CCAGGTCAG TGGTTCCTGC TGTGGGACTT 50

GCGTTTTTAC TAAGTGTTGGC GTTAGATCCA TTAGTTCCCG AAGAGCCTCC 100

20 AGTGCTTCCT AATGCCCCCA AGCCAGGAGT AAACCCTGGA ATGAGGCCCA 150

GGGCTTCTAT TGCTAATGCC TGTAAACCTT GCTGAATCTA TAACAGAGTC 200

25 TATACCGCTC TCG 213

(2) INFORMATION FOR SEQ ID :879:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 227 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :879:

AAAGAAGGAA AAGAAAGAAA TAACACTTAA CAGTCCATAA CAAAGTGTTA 50

40 ACGAGATAGA CACATGCTTA TTCAACCAC AGATATGATC CAGTTAATTC 100

444

CCTTCTTAGA ATGTGCCCCAT AGTGCCTTAT TGCCTCATAA TAATGATAAT 150  
AATAAGAGCA ACAATAATAA CGGCACAAAC TCCAGTCGAT ACTGACAAAC 200  
5 TACCAGAGTA ACCGTCATCC CCTTGAG 227

## (2) INFORMATION FOR SEQ ID :880:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :880:

ATAGACAAAG TCCTTCCCAC TAGAACTTAC ATTCCAGTGG GAAGAATTAG 50  
20 AAGCCTCAGG AATTCCATTG CTTACTTTTA GTTGTTACTT CAAAAGTACT 100  
TACATTTAAT CTGATTATTA ATTATTCGTC ATGAGCTTCA TTTTATTACA 150  
25 TCCAGGGCAC AGTATGTGAA TTGTGTTTCG TTCCTTTAGG AAAAGGAAAA 200  
ATAATCACTC TTTACAAGGT A 221

## (2) INFORMATION FOR SEQ ID :881:

30

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 310 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :881:  
AATTGTGGTA TATTTCAATTT AAAATCGATC AAAGACAGCA ACATACATTA 50

445

ATCAGAGGAA AGCATCAATT AAATGCAGAA ACAAGATTTA AACAAAGATT 100  
CATATTAAAA CAATGATAAG TAATACTTAG AAAGTGCATC CTAGAGACAC 150  
5 ATCATTGCGA TTTTGTAGAA AACAGAAACA TATTAGTGTG AAAAGATGTT 200  
AAAAAATGAA TATTAAACCG TCGAGCACAA CAACTACGC CGATAACAAT 250  
ACACCACAAG CGCCGTAATC CTGCCGACAC TGACACACTA CAGGCGTCGT 300  
10 GGCGATCCGA 310

## (2) INFORMATION FOR SEQ ID :882:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 177 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :882:

25 GTTCACATCA GTGTGTAGGA TATGCTATCA CGTATGTGCA TGAGAAGAAT 50  
GGAGAAAATG GATCTATGCG GATGTCTGTA CACACACACA CACACACATA 100  
CACACAAGC TTGCACATGT ATAGAGGATC CGAAATTCCA CCAATACTGA 150  
30 CGAACTACAA ACGTAACAGC AGCAGGC 177

## (2) INFORMATION FOR SEQ ID :883:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 152 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

446

(xi) SEQUENCE DESCRIPTION: SEQ ID :883:

CAATTCTATT TTCAGAGTTG ACTGTACTCT TTCCTCTGA AGATACACGT 50  
5 ATAAACGCGA CCAACGAGGT CTCTCGTCCT AATAACAGGT TCAGGCATGA 100  
ATCACCGTCT AACAGCTATT TAAACACCGC CTCTTCATAG AAGTAACGCC 150  
GA 152

10

(2) INFORMATION FOR SEQ ID :884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 177 base pairs  
15 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :884:

GCATAATATA AGTATTTATC ATGTATTCTG TGTCTGGAAT ACAATTCAAT 50  
25 GACCTATTTC AGAAAAATCT TTTCAAGTAC TGGCTGAAAG AGTGAGGGAT 100  
ACATTAGGAG ACTGCAAATA AACTGGCAAT CACAAGAACT TTTTCGGATA 150  
AAATGAAATT GTGCCGAAAT GTATACA 177

30

(2) INFORMATION FOR SEQ ID :885:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs  
35 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :885:

447

5 CACAGCTGGA AGAGCGGAGA AATAGAATTG TCTTCAAACA ATATAAAAT 50  
TCATAAAGAA TAGAAAGACT ACTATGTGTG GGTCGGGAAA TTAAC TAGAA 100  
TTTTTTTATA TCCACACTCT AGTATGAAAT GAGTACTTAT AGAGTAGACT 150  
GTAACATATT TAGACATAGT ATATATATAT ACAAGTGTA CAAATATATA 200  
TATTAAATAT ATATATGTTT TATAGAAACA CAGAGCACAC A 241

10

(2) INFORMATION FOR SEQ ID :886:

(i) SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 190 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :886:

GTAGCAACCG GCGCTCAATA AAATTCAACC AGCAAAC TCG ACAAGTAACA 50  
25 ACCATAAAAC CAGCCACACT AAGTCCAGCC ACCACTACTC AATAAAAATA 100  
ACACGTATCT TCCACCGTAC AACCAATAGC AACTGCAGGC TACTGCAACG 150  
CCATCCATAT ACCAAAAATG CTACTTACAA CACCACAACA 190

30

(2) INFORMATION FOR SEQ ID :887:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

(xi) SEQUENCE DESCRIPTION: SEQ ID :887:

448

CACGCTTTCT CTCACACAGC ACTAGCGCTC TCTCACTATC ACTCTTCTCA 50  
CAGAGCTGCG CGCGAGTCTC ACTACTATCA AATATATCTG TCTCTTCTCA 100  
5 CTCTATAGCT CTCTCACAGA TATATATCTA CATATAGCGC TCTCATTATA 150  
CTATAATATT ATACTCTC 168

## (2) INFORMATION FOR SEQ ID :888:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :888:

20

ACTGGGCGCG CTGGTGCTGA CATCTTCAAG AGCATCTGTC ACTGAATATT 50  
GCCGATCTCG CAACCGGTTC CAGTTAGACA GAACATTGTG ATATTCAAAC 100  
25 CACTTTCTCG TAATTTCCAA TGGAGTTGTA AAGTTTAATG AGACCTCGAT 150  
AATCATATTG TAGTCCACTG TAGC 174

## (2) INFORMATION FOR SEQ ID :889:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :889:

40

ACACCACACT TAAGGAATGG GAGTTATATT TCACTTCCCT GAGGCCAGAA 50

449

TATATATATG TATGTATGTA TATGTGTGTG TGTGTCTATA TATATATATA 100  
TATAGACACA CACGCACATT ATACACACAT ATATATACAC ACACATATAT 150  
5 ATATGTGTGT GTACAATATA TAAAAAATTA TATGGGAGAA AAGAAAGGCA 200  
AATCTCCCAT GGCAGAGAGG TATCCCAAAA AATTTTTTTG TGTGTAACAA 250  
AATATGTTGT GTGTATATAT ATATGCACAC ATATTTATGT GTATATATGT 300  
10 ATATATATAT CTGTATATAC AGGTATA 327

(2) INFORMATION FOR SEQ ID :890:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 181 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

(xi) SEQUENCE DESCRIPTION: SEQ ID :890:

25 TTTTTTCTT GTCTCTCCCG CAGCGCGCGC CTCTCGCGGC GCTATCTCTC 50  
GCTCTCTCTC GCTCTCTCGA GCTCTCGAGA TATAGCCGAG ACACGAGAGC 100  
TCGCTCTCTC CCGCGCGAAG ATCTCACCCC CGCGCGCTCG CGCGATATAT 150  
30 ATCTCCTCGC GCGCGCGCCG AGCGCGCCCC T 181

(2) INFORMATION FOR SEQ ID :891:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 207 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
40

450

(xi) SEQUENCE DESCRIPTION: SEQ ID :891:

|    |  |     |
|----|--|-----|
|    | CTCTTTAATA GCAAGCGAAT GGTAATTACA TGGTCCGATG AGGTCCTCAC | 50  |
| 5  | TCTCAGGGGA GGGAGGAGGG AGCAGAGGTG GACAGGGTGC AGTATAGGAT | 100 |
|    | TTACACTGTT TGAAGCATCT AACGAAGGGC AACAGTTTTT GGCAACCCAA | 150 |
|    | TTCACAGTTT TGTAATTTAC AAGAGATTTC TTTGAAAGGA AATAGGAAGG | 200 |
| 10 | CAAAGAA  | 207 |

(2) INFORMATION FOR SEQ ID :892:

|    |                               |
|----|-------------------------------|
| 15 | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 198 base pairs    |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |
|    | (D) TOPOLOGY: linear          |
| 20 |                               |

(xi) SEQUENCE DESCRIPTION: SEQ ID :892:

|    |  |     |
|----|--|-----|
| 25 | CTATCACTTC AGGGAAACAA ACAACTAACA GCCATCAATT CAGAGGGAAG | 50  |
|    | TGATTTTACA GTAGAGTGAA CGAACTTGG GAAGGAAAAC ATCCAAGAGG  | 100 |
|    | CGTCTGTTTG ACGTGGGTAA CGTGGGGAAC GCATACTGTC TGGCAAGAAT | 150 |
| 30 | TCTACTAGGA CCACGGGAAA CAAAGCAGAT TAAACACTC TCTACTCT    | 198 |

(2) INFORMATION FOR SEQ ID :893:

|    |                               |
|----|-------------------------------|
| 35 | (i) SEQUENCE CHARACTERISTICS: |
|    | (A) LENGTH: 96 base pairs     |
|    | (B) TYPE: nucleic acid        |
|    | (C) STRANDEDNESS: double      |
|    | (D) TOPOLOGY: linear          |
| 40 |                               |



451

## (xi) SEQUENCE DESCRIPTION: SEQ ID :893:

CTTTAGAGAA TGCCTTGTGG AAAAAAAAAA AAATGGGCCC CAATACTTTT 50

5 TACTGCCCTT TATCAAAATT GTTGTGCATG GACCGGGCCA AATAAG 96

## (2) INFORMATION FOR SEQ ID :894:

## (i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 325 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID :894:

AATTGTATAC CAACATATAA ATTAAAAGTG TTATGCAATG AGAAACAATA 50

20 ATGGAAACAG CATAATACTA CATACTATCG CGCGGGGTTG TCGGCGTGGT 100

GGGCGTGCGT GTAGAGAGAG AGCAAGGGCG TGTGCGTGAG TGGGCGTAAA 150

25 GAGTGAGCGT GGGAGGGTGT GGTGCGTGGA GGTGTGTGGA GAGGTGAGTG 200

TGCGAGAGGG GCGAGTGTAT GTGTGATAAG TATAGCCCGC AAGAGGCCGAG 250

GACAAAATAT ATATATATAT AGATATAATA GATATGAGAG AACACTAAAC 300

30 AATAACCACT ACTCACATAG AATAT 325

## (2) INFORMATION FOR SEQ ID :895:

## (i) SEQUENCE CHARACTERISTICS:

- 35 (A) LENGTH: 266 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

452

(xi) SEQUENCE DESCRIPTION: SEQ ID :895:

ATAGTTGTAC ATTTTATGG GGTGCATGTG ATATTTTGAT ATGTGCATAC 50  
5 AATGTGTAGC AATCAAATCA GGGTAATTGG GATATTCATC ACCTCAAACA 100  
TTTATCATTT ATTTGTGTTG GAAACATTCA AACCTTTTCT TCTAGCTATT 150  
TATCCATTGT TGGATACTTA TATCAATTCT ATATCTTAGC TGTGTGAAT 200  
10 AGAGCTGCAA TAAATGTAGG AGTGCAGATA TCTCTTTGAT ATACTGATT 250  
TCTTTCTTTT GTTATA 266

15 (2) INFORMATION FOR SEQ ID :896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :896:

AAGAAGAGTC TTCTGCACAA ACAAACCAT AGTGTTGACA AATAGTCATG 50  
GCCAATGGCA ATCTGATGGT CCAGCGGCCC TCGGATGACT CCTCTGCAAG 100  
30 GAGCATCTTC AGGGTTCTAG GGAAGTCACA GGGGCAACAT ATTGGAACT 150  
AGCAGGCCCA GAAGACCGCC CCGCCCCCA TGCCCTGGCG CAGGGCC 197

35 (2) INFORMATION FOR SEQ ID :897:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

453

## (xi) SEQUENCE DESCRIPTION: SEQ ID :897:

5 GATGGCTGGA GTAGATTAGG GCGTAGGTAG AAGTAGAGGT TAAGGAGGGT 50  
GATGGTGGAC TATGATGGTG GGGATGATGA GCGCTATTGT TTTTGTGAA 100  
TATTTTCTT CCGACTAACT CGCGCCCCAC TCTCTTGCGA GCACAAACAC 150  
10 ACGCGCGCGT GTAAGCGGCG CGAGACACGC GCCCCTTCCC CT 192

## (2) INFORMATION FOR SEQ ID :898:

## (i). SEQUENCE CHARACTERISTICS:

15 (A) LENGTH: 224 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :898:

25 TGGATGTTTT CATTGCAAAA TCATGAGAAA CTTAAGTGGG TTTTATGCAC 50  
TTGATAGAGT TGGCAAAATT GAACTATGAA GTTAACTATT TAACTCAAGG 100  
AATGGGCGGC AAACCCATCC CCTCGATTGA TAAAGAAGGG GAACATTTTT 150  
30 ACATTAGAAC TGACACTGAA AACATAGCTC TTTTTCAGTC CACCCTGGTT 200  
GCTCTAGTAG CCCACAGCCC AATC 224

## (2) INFORMATION FOR SEQ ID :899:

35

## (i) SEQUENCE CHARACTERISTICS:

40 (A) LENGTH: 362 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

454

## (xi) SEQUENCE DESCRIPTION: SEQ ID :899:

|    |  |     |
|----|--|-----|
|    | GAGGTGATTT CTCAGAGTTT AGAGAATAGG ATGGGGAAAA TTATATTTAG | 50  |
| 5  | TGAGTTATAA CCAGAATTAC ATAAGACAGA TATGGAAATT TTATAAACAA | 100 |
|    | AATGCAAAAT ATTCTAATGT TTCAATGTTC TACATGAACA TATAGGGAAG | 150 |
|    | CATAGACAAT AGCCAAAAAT ATGTTCTGCA TTCATATACT AGTTCAAGTC | 200 |
| 10 | CGAGTCTGGC TACTTTCTAG GTAGTGTGCT TTTTGTCAA TTATAAAGAT  | 250 |
|    | ATATTCCCTT TGTTTTTTGA AAACGAGTGA GATGCTTAA TAGAGTACAA  | 300 |
| 15 | TTATCTCATT CAAAATGTAT GTTGTTCCT CTCGAGAATT GTGAAGGTTT  | 350 |
|    | TGAGATTGA TT   | 362 |

## (2) INFORMATION FOR SEQ ID :900:

20

## (i) SEQUENCE CHARACTERISTICS:

- |    |                            |
|----|----------------------------|
|    | (A) LENGTH: 310 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
| 25 | (D) TOPOLOGY: linear       |

## (xi) SEQUENCE DESCRIPTION: SEQ ID :900:

30

|    |  |     |
|----|--|-----|
|    | GTATGTAGCC CAGTGGGTGT CTTCCACAG GGTAGGTACT CAGTTTGCTC  | 50  |
|    | TGGAGGGTGA CTCATACCTA AACAAGTGCA CATCTCCTTT CTCAGTAAAG | 100 |
| 35 | CCAAAGCAGG TTTCTACATT TGGAACAAAA GAGATCCTGA CCAGAGAGCT | 150 |
|    | ATCACTGGTG GTCCACTTGG GCCCTCCTTG ATGGGTGTGT TCACTTAGAA | 200 |
|    | AACCAAATTA CAGATCTGAA GGCTGCTGGG TAGGGACAGG ATTAGAACAA | 250 |
| 40 | AGGGAATGAG ATTGAATGTT ATTTAAGGGA TATTTCTGTC AAGTTTTGGT | 300 |

455

TTCTCGATGA

310

(2) INFORMATION FOR SEQ ID :901:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 185 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :901:

15 TTCCCCCATG AGACCGTTAG TCTCTCTTTG CCTGGCTGAC TACCTGCATA 50  
CAGTAGGCAC TCACTGCTGG AGTGAGGCAC TGA CTCTCC AAAGATTGCA 100  
GGGGGCGGAG GAGGGAACCA CGAAGGCCTG GGAGGGGGCA TCTTTGGCCC 150  
20 CCACTAACCA TCTCCCTATT TCTGCATCCT GGTGA 185

(2) INFORMATION FOR SEQ ID :902:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 381 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :902:

35 ACAAGCTGCA AGATCCTTCA CTTGAGGCTT TCAGCCTTAT TCTCCTCCTG 50  
TCAAACA ACT AACTACTCC GATGTTTGAT GAAAATTAAA CTGCTACTCA 100  
GGATACTGCA ATTACAAGGA GAGGGAATGA TCAGCCCAGG GAGGCTATTA 150  
40 CGTGTGACCT TTGAGATGGA CCTGATCGCC CCTTTTACTT TTTAGACTAC 200

456

AAGTGCAGGG AGGTGGAGCT TATTTCATT TGAACCTCTG TAAAGAGTAA 250  
GAATATGGAA AGGATGAAGC CTCATTCATT CGGGCATATT AAAAAGAAAT 300  
5 TGCCTTCAGA AACACTTTGC CTTTAAATAT GTGTAGCTAC AGTAAGTACC 350  
AATGGGCTAA CTAATTGAAG CTAACATTTT A 381

## (2) INFORMATION FOR SEQ ID :903:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- 15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :903:

20

CATCAAGGGT TTTTCCTGCT GCAATTCTTG TCAAAAAGT ACATATGTAT 50  
ATCGTTCTCA ACTGGCAAGC TGTTAGACTG GATAGTCCAT GAATAATAGC 100  
25 CTCTGCGCTG TTGCGGGTCC TCGGAAGTC CTCGGAGCGG CCGTCGCGGA 150  
AAGCTCGGCA AAGAGAGAGG CAGAGGAAAT CGAGCATCCA GCCGGCAGCC 200  
ACTTTTTTTT TATCGGCACC AGGCCGCGTC CTCTCTCTCC 240

30

## (2) INFORMATION FOR SEQ ID :904:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 280 base pairs
- 35 (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

40

## (xi) SEQUENCE DESCRIPTION: SEQ ID :904:

457

CCCTGGGCAG GCTGCTGGTG GTCTACCCTC GGACCCAGAG GTTCTTTGAG 50  
TCCTTTTGGG GATCTGTCCA CTCCTGATGC TGTATGGGC AACCTAAGG 100  
5 TGAAGGCCTC ATGGCAAGAA AGTGCTCGGT GGCCTTTAGT GATGGCCTGG 150  
CTCACCTGGA CAACCTCGAA GGGCACCTTT GCCACACTGA GTGAGCTGCA 200  
CTGTGACAAG CTGCACGTGG ATCCTGAGAA CTCAGGCTC CTGGGCAACG 250  
10 TGCTGGTCTG TGTGCTGGCC CATCACTTTG 280

## (2) INFORMATION FOR SEQ ID :905:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 225 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :905:

25 GTTCTAGTGG TAACTGCTGC TTCTGGAAAA TATTAGAGA AACCAACGGT 50  
AAAAAAAAAA ATAATAATTA ATACCGTTGG TTTCTACATA CACTCTCAAT 100  
ATTTGCACGA GTAAAGCGTA GCAAGTTTAA CACAATTAT GTAAACTTGG 150  
30 AAAATTTTCC GAAATTTTAT TGAATTTTCT CGGTCTCTCC TATCTTTATA 200  
TACACATCTC TCATGCACAC ACGCG 225

## 35 (2) INFORMATION FOR SEQ ID :906:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 161 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

458

(xi) SEQUENCE DESCRIPTION: SEQ ID :906:

|    |  |     |
|----|--|-----|
| 5  | GGTGCTGACA TCTTCAAGAG CATCTGTCAC TGAATATTGC CGATCTCGCA | 50  |
|    | ACCGGTTCCA GTTAGACAGA ACATTGTGAT ATTCAAACAC TTTCTCGTAA | 100 |
|    | TTTCCAATGG AGTTGTAAAG TTTAATGAGA CCTCGATAAT CATATTCTAG | 150 |
| 10 | TCCACTGTAG C   | 161 |

(2) INFORMATION FOR SEQ ID :907:

(i) SEQUENCE CHARACTERISTICS:

|    |                            |
|----|----------------------------|
| 15 | (A) LENGTH: 204 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

20

(xi) SEQUENCE DESCRIPTION: SEQ ID :907:

|    |  |     |
|----|--|-----|
| 25 | AGAGATATAT GCAATCTGGT AGTCCATTAA ATGAGAGTTA CACTTAAAT  | 50  |
|    | ATTTTAGTTC TTTTAAAGAA AAAGTCTCCA TGTGCTATTT GGGAAAACCT | 100 |
|    | TCATTGCCTA AAGACCCACT TGCATAATTA AGGCAGATGA TGATGATCTT | 150 |
| 30 | TATATATGCG CACACACACA CACACACGAC ACGACGACAC ACACACACAC | 200 |
|    | TCTA   | 204 |

(2) INFORMATION FOR SEQ ID :908:

35

(i) SEQUENCE CHARACTERISTICS:

|    |                            |
|----|----------------------------|
| 40 | (A) LENGTH: 316 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |



459

## (xi) SEQUENCE DESCRIPTION: SEQ ID :908:

|    |  |     |
|----|--|-----|
|    | AGTTTCTGCA TTTGGTCTGT GTGACTCTAT GGAGCCCAGG ACTTACAGAA | 50  |
| 5  | AAAGGTGTAA CTGGCTCTTA GGACTTTAAG CCACATTATG GTAGTAGACC | 100 |
|    | TGCCGTTTTA TTTGACATGG TGAAATAAAC TACCACTCCT TTGTGGTACC | 150 |
|    | ATATGGGCAG GACAGAGCTC TTCAACCCTG GCTAACAAGC CTGAAGAAGA | 200 |
| 10 | CCCTGTGAGG CCGCAGCAGC CATGGGAACT TCCCAAAGGA CAGAAATCCA | 250 |
|    | CATTGGAACG TAGCATCCAG ATAGGTGACA GAAATTCCTT CCACCATATC | 300 |
| 15 | CAAATGTGTG TGTTTT                                      | 316 |

## (2) INFORMATION FOR SEQ ID :909:

## (i) SEQUENCE CHARACTERISTICS:

|    |                            |
|----|----------------------------|
| 20 | (A) LENGTH: 307 base pairs |
|    | (B) TYPE: nucleic acid     |
|    | (C) STRANDEDNESS: double   |
|    | (D) TOPOLOGY: linear       |

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :909:

|    |  |     |
|----|--|-----|
|    | CTAGTAACAT AGAAAATAAA CTTCAGTGGG AATCTCTGCT TCCCGCGTGA | 50  |
| 30 | GGTGTTTAAT TCTTGCCATT TTTGTATTTT AAAGATGTAG CAACTTGTTT | 100 |
|    | CAAGTTAGAG GAGATGGCAG GGTCAAAATT TTAGAAACTG GATCCCACCA | 150 |
| 35 | CCACTGTGTT ACTTCCTAAA CCTGCATACA AATGTTCTGC CAACATGTAA | 200 |
|    | TGTGCCAATA GAATTATACG GTGTGAACTG CATATCTCAG TATCTCCACG | 250 |
|    | GGAAAAAACT GTGGTTGGGG CATGGAGGGG GGAAAGGGAA ACTTTTTTAA | 300 |
| 40 | GCTATTT  | 307 |

460

## (2) INFORMATION FOR SEQ ID :910:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 172 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :910:

TTTTTTTTTT TTTCCAGGCA CCTAACGATT TGTTTGTCTC AATCAAACGC 50  
15 AGACAGGCGT CTCCGAAGTA CCACCACTGG GATATCCTCG GACCAGCGCT 100  
TAAACCGAAT CCCACAATC TCAAACCTCAA CCAGGCCAAA GGGAACACAG 150  
TGACACAACA ACAGGGTTCC AA 172

20

## (2) INFORMATION FOR SEQ ID :911:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 255 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :911:

GCATAGAGAG ATATATACAC AGAGAGGACA TACATATATA TATATAGAGA 50  
35 CACAGAGACA GACATATAGA GATATATATA TACACAGCAT AGAGATACAG 100  
AGAGATAGAG AGAGATACAC ATACACACAT TCATCAACGA GAGAGAAGAG 150  
AGGAAAGAGA GAGAGAGCGA GCACAGACAG AGATAGAGCA CACAGAGAGA 200  
40 TCGCGCAGAT CTATACAGAG GGATATTCAC CACATTGTAT ATGGAAAGCG 250

461

CATCT

255

## (2) INFORMATION FOR SEQ ID :912:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 196 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :912:

15 CAAGCGAATG GTAATTACAT GGTCCGATGA GGTCTCACT CTCAGGGGAG 50  
GGAGGAGGGA GCAGAGGTGG ACAGGGCGCA GTATAGGATT TACACTGTTT 100  
GAAGCATCTA ACGAAGGGCA ACAGTTTTTG GCAACCCAAT TCACAGTTTT 150  
20 GCAATTTACA AGAGATTCTT TTGAAAGAAA ATAGGAAGGC AAAGAA 196

## (2) INFORMATION FOR SEQ ID :913:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 203 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :913:

35 ACTATCACTT AAGGGAAACA AACAACTAAC AGCCATCAAT CCAGAGGAAA 50  
GCGATTTTAC AGTAGAGTGA ACGAACTNG AGAAGGAAAA CATCCAAGAG 100  
GCATCTGTTT GACGCGAGCA ACGCAAGGAA CACATACCGT CTGGCAAGAA 150  
40 TCCCACTAGG GCCACGAGAA ACAAAGCAAA TAAAACATT ATCCACTACA 200

462

CGA

203

## (2) INFORMATION FOR SEQ ID :914:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 262 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :914:

15 CTGCCGAGCC ACCATGCTTG CCTGAAGCTT CGGCCGCGCC ACCCGGGCAA 50  
GGGTCCTCTT TTCCTGGCAG CTGCTGTGGG TGGGGCCCAG ACACCAGCCT 100  
AGCCTGGCTC TGCCCCGCGAG AACGGTCTGT GTGCTGTTTG AAAATAAATC 150  
20 TTAGTGTTC AACAATAATG AACAAAAAA AAAATGATAA AAAAATCGGA 200  
TTTCCGGTTA AACTGTGAC TTCAATTGAA ACACCTTTTT GTAGTATCTG 250  
25 GAGGTGGACA TT 262

## (2) INFORMATION FOR SEQ ID :915:

- 30 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :915:

40 TGGGTTCTAA TGATGTGCTT GAAGAGGAAG ATTTTGATCG CACCACTGAT 50  
ACACGGAGTC TGTATTTTGC ATCCTAGAAT GATTAACCAG AAACAAAGAA 100

463

AGGAAAAAGG TAAAATCAAT AATAAGATCA GCAGCTCTGG GACACAGAAT 150

AAAGAATGAA ATAATTTGAA AAAAAAGGCA GGGCAGGCAA A 191

5 (2) INFORMATION FOR SEQ ID :916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 252 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :916:

AGACTTGGGG GTTCCTGGTG TGTGAGGGGT CCTGGGATAG CTAGGGGTTT 50

TCCAGGAGTT GTCCTTTGTT GTTGTGCGTG AAGAATTATA CTTGTGTGT 100

20 GTGTGGGTTG TCCCATGTGT ATGCGTGTAG TGTGACAGTA TATGACCCCC 150

AGTGTGTGCA TATGTTTGTG TGTTGTCTC TGAGTGATAT CCACCTCTCT 200

25 CTCCCCCTCT GTCTCTCTGC AGAGATATGT GTGGCGTCAC TGTACTCTTG 250

TG 252

(2) INFORMATION FOR SEQ ID :917:

30

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

35 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :917:

40

TAGACAGAGT GACAGTGAGA GAAAAAGAGA GGAAGGAAAA GGGAAAAGGA 50

464

GTAGGGAAGG ATGAGGGAGA TAGGAAAGCA CCTAC GAG GCAGAGAGTT 100  
TCCTGAAGGT CATGCGATCC TTTACCCTCA GAAACTTTCA GGCTGAAATC 150  
5 ACCATCTCCG TTATCCCAAC AAACGCACTC TCCTACCTCT ACAAGCACTT 200  
CAAGTAAAGC AGAAATCACA CCAATACTGA CGNGCTTCAA GCGCAAC 247

## (2) INFORMATION FOR SEQ ID :918:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :918:

20

ATTGGAATTC AATTGCCTGT TGCACTTTTA CATTAGTGT TGCTTAAATA 50  
AACAAAAATA GAGCATAAAT TCAATATTCT ACTGTCTAAA CATTTTAAAG 100  
25 CAATGGTTAT GCCATCATAA ACAAGTAAAA TGCACCTAAT TCGAGTCTTT 150  
TGACACCTCT TGTTTTAAGT TTCCTGTATG ATAAAGTTCT T 191

## (2) INFORMATION FOR SEQ ID :919:

30

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
35 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :919:

40

CAAGAGTGAG ACTCCATCTC AACCAAAAAA AAAAAGAAAG AAAAAAAGAA 50

465

ACAACCTCCT CATTTTCAGA AGCGAACACA CCCCCGCCCC AAGATAGACG 100  
ACAGAGACCG GACTAAGATT TAACCCAGGA ACTTTTCGCT TGGGCACCTT 150  
5 CGAACAACAC ACAACCCGCA AAACCATACA CGCTCCCTTG CCCGAGGCCC 200  
AACCC 205

## (2) INFORMATION FOR SEQ ID :920:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :920:

20

GACAAAATTG GGACTCTAAG TATTGCGCTT TTTTTCCTC TCCAACGACT 50  
CGTTCCCTTT CAACAAATAG CACTTCAGTC CACTGTGTAC AGAAGTAATA 100  
25 CATCTCCTAT CGTTAGTTGA ATAAATTCAC ACACCGCGTT TAAGAGATGA 150  
AACCACGACT TCGTCAAGCC ACATTCGATT GCCATAAGAT TCCAAAGAAT 200  
TCTATCCTCT TAAAGCGAAC CACATGTAAC CCGAAGGTCC CCACCTATCA 250  
30 AGGTTAGAAC TGATATTCAA ATTATAGACT CATTCCACTA AGCAAGTAAG 300  
CTCTAAGCTA CAGGTTGATC ATA 323

## 35 (2) INFORMATION FOR SEQ ID :921:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

466

## (xi) SEQUENCE DESCRIPTION: SEQ ID :921:

5 AACATTGACG ACGCTAAGGA TGCCATGATG CCATGAATGG GAAGTCTGCA 50  
GATGGACGGC AGATCCGAGT AGACCAGGCA GGCAAGTCGT CAGACAACCG 100  
ATCCCGTGGG TACCGTGGCG ACTCTGCTGG GGGTCGGGGC TTCTTCCGTG 150  
10 GGGACCGAGG CCACGGCCGT GGA CTCTCTA GAGGCGGCGG GGATCAAAAC 200  
TATAGAAACA ACAAGTTAGA GTACAGACGT 230

## (2) INFORMATION FOR SEQ ID :922:

15

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :922:

25

TATTTTCTCT GATGTTCTCC CTCCTCCAG TCCCCGACCT CCCACAGGCC 50  
CCAGTGTGTG TTGTTCCCGT TCCTCGTGTC CGTGAGTTCT CATTGTTTCA 100  
30 TGCCCATTTCT GAGGGAAAAC ATGCCAGTGC TTTCGCGTTC TTCCTCGCTC 150  
TCACCCACCT CTCAGCTTAT CGCGTCGCGC GCGCAGTATA TTCGTCTCTC 200  
TCTCCAGTCT CTCTCGCGAC ACACATCTCT CTTTTGTAA 239

35

## (2) INFORMATION FOR SEQ ID :923:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 base pairs  
40 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear



467

## (xi) SEQUENCE DESCRIPTION: SEQ ID :923:

5 GTCAGTTCAG TTGTGAACAA AGCCCTTTGT GTACGTTTTT AAATTTTAGT 50  
TCACACGATA ACAATGCTTT GCAAGTAGGT GTAATTATTT TACTCCCATT 100  
TTATGGATGA GAAAACAACA GAGAGGTTGA TTGGCCCCAC CTTCAAATCC 150  
10 TGAAACCCGT CCACTCAATA AATTTTGT 178

## (2) INFORMATION FOR SEQ ID :924:

15 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 325 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear  
20

## (xi) SEQUENCE DESCRIPTION: SEQ ID :924:

25 CAGCTGGTCC CCCACTAAAA GAAGGGGCAG ACCACCACTA GCCAAAAGAG 50  
ATAGCAAGAC TAACATCTGG AAGAAGCGAG AGGAACGCCC ACTGATTCCC 100  
AAAAAAAAAC TCCAATGGGG ATTGTGTGTC TGCTGTCTCG TGCTGTTTAT 150  
30 TCTTGCTTCT TGTGTAAAT TGCAGTACGA ACTTAAGAAA ATGAGACTGA 200  
GCAATCTCAT GGTTCCTGGA CATGTCTCAA GCAGAGTAAA TGGTAATTCA 250  
35 GTAATCAGAG AGAAAGATAC CAAGGAATGC TTTTCTGGC CTATTCATT 300  
ATTTTGGGG GATGAATTA CAGTA 325

## (2) INFORMATION FOR SEQ ID :925:

40 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 261 base pairs

468

- (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :925:

ATGGCTATGA CCTGGGACAT GGAAACAGTG ACCTCCGCGT TCTGGTCCCG 50  
10 AGATCCTCGC ATCAGCGTCA TCGTGTGCAC CGGCTTGGGG GGCTGGAGTT 100  
CCGGTTTTCT TTGTTTTTTC TCTTTATTCG TCCTTTCTCA AAGATGGGAT 150  
15 ACTGATCAGA ATCGTTCTGT ATATGCTTGG GACTGGATGG AAAGACTTTG 200  
AAGCAGCTGT GGGGGGCGGG AGGACACCGA CAACCAAACA GACGTGTTGG 250  
TTCCAGTCCT G 261

20

## (2) INFORMATION FOR SEQ ID :926:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 base pairs  
25 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :926:

GTCAGCCTGG GCAATCACAA CGACAACAAA AGGTACAGTC TCAAGAGTCC 50  
35 AACTGGGTTC AAATCCTGGC TCTGTACAT ACTAGCTGTG TGACCTTGGC 100  
CAAGTTTCTT AACCTCTCTG TGTGTATAGT CCTTATCTGA AAATGGGGAT 150  
AACCAACCAA GAGAGCTGAG AGA 173

40

## (2) INFORMATION FOR SEQ ID :927:

469

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :927:

10

AACACTCAGA CCGGACGGGA CGAGGGATTC CCCTGCCTTC GCTTCCCTCC 50  
CTCGCTTGCT TTGTAGTTTT CCCGCACCAG CCCGCTGCCC TCGGCCATCC 100  
TAGGGCCTCG AAGCCCGGGG AATCTGTCCC ATCCTGTAAC GGGCCGCCCC 150  
CTTGATTTT TCTGCCCCGTG CCACCGGAGG TTGCTGCGAC GCGCACCGAC 200  
TCAGATCATT ACTACTGAAC TCG 223

20

## (2) INFORMATION FOR SEQ ID :928:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :928:

35

GTTATAATTA TTTACATGCT GCAACACGTC ACAACATAAA TTTACCAAAT 50  
ATTCATGGT GGGATGCTGT AGGTTTCAGA TAATAGTTTT AAGATAAAAA 100  
CCACAGATTA AGTGAAGACA CCCACAACCT TAATGACTCT ACGACTCTCG 150  
GTTGCTAAAT GCTAGAAGTC AAAAGGCAGT GTTTTTTCAG TCCTACCTGT 200  
CATAACTTGC AT 212

40

470

## (2) INFORMATION FOR SEQ ID :929:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 233 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :929:

TTAACATAAT ATTTTGAATA TATAGGGCTC ATAAGATATA TTATTAAATT 50  
15 ATAAACAAAA TAATCAGGAA CTTAGTGTGG TGCCTAGTTT GATATATGAT 100  
TACTTTTTGA AATGCACTAA ATTCCACAAA TAATGAAAGT ATTCTTTGTG 150  
TATAATGTTA TGTTTGGTTA TTATGTATGG TCTTCGTATC CAAAGGTATG 200  
20 ACATAACTTG AGTTTGTITG CTGCTATTT ATT 233

## (2) INFORMATION FOR SEQ ID :930:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :930:

35 AGTCTGTAAC GATACACCCA TAGATGTGAA TTATGTATAT TCGAGAAGGA 50  
GATCAGATGG CATCCAGAAG ATAGTTTAGA TTTCAGCACA TTCATGGTTC 100  
AGATGCAAAA TCAGATCATC AAATAGATCC AGCAATTCAC AATCATCATA 150  
40 GCCATATCGC GTCACGTCCG CCGCACAAAG ATCCGCACCA ATTATCTATC 200

471

TCCCACCCCC CCCAGGCATT CAGCACCCGC AAAAG

235

## (2) INFORMATION FOR SEQ ID :931:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 221 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :931:

15 CTATCTAGAA TTA CT TATTT CACTGAAAT GTATGGTTTC AGGAAAATTT 50  
TCAATTTAAC TTGAAGGGAT TATCTTTAT TTTGCTTGA ATAATGGCAT 100  
CTCAGAAACA TGGGTTTACC TGTGATTTTT TTGTTGGGT GAATGCTTAA 150  
20 AAACAAAAA AAAATTTACA TATGCATTTT ATGGATACAC ACACACACAC 200  
ACACACACAC ACAAAAAACA C 221

## 25 (2) INFORMATION FOR SEQ ID :932:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 333 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

## 35 (xi) SEQUENCE DESCRIPTION: SEQ ID :932:

TGCTCTATTG CTATCTCCTG ATATAGGTTA TATATATATT ATGTCTTGAG 50  
CGTCATGTCT TGTGCTACTA CACCGTGTTA ATCCCAGCTA CTCAGGAGGC 100  
40 TGGAGGATCG CTTGAGCCCA GGAGTTCTGG GCTGTAGTGC GCTATGCCGA 150

472

TCGGGTGTCC GCACTAAGTT CGGCATCAAT ATGGTGACCT CCCGGGAGCG 200  
GGGGACCACC AGGTCTGCCT AAGGAGGGGG TGAACCGGCC CAGGTCGGAA 250  
5 ACGGAGCAGG TCAAACTCC CGTGCTGATC ATGTAGTGGG ATCGCAGCCT 300  
GTGAATTAGC CACTGCACTC CAGCCCTGAG CAA 333

## (2) INFORMATION FOR SEQ ID :933:

10

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 281 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
15 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :933:

20

AGATTATGG CTGCTTTCAC TTGGCTCCAT GTTCTGCTGA TAATTAAACA 50  
GTTTGTGTGT CCTGTCTTTC CTCAAAGGAA CTGTCAACC TTGGAATTT 100  
25 TGTTCATCTC AGAGGGACGT CTTAAGTACT CAGCTTCTG AATGTTTAAG 150  
AAAAAAATAA TACTTTTCAG AATTACCTAC CTCTTCTCA TTTTAGCCT 200  
GGGATCAATT ATTCCCTTTC ACACTTTTTT ACATCCTAAG TAGAAATAAA 250  
30 ACTCTTTATT CTATTTTTTT TCAGTTATTG G 281

## (2) INFORMATION FOR SEQ ID :934:

35

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
40 (D) TOPOLOGY: linear

473

(xi) SEQUENCE DESCRIPTION: SEQ ID :934:

AATCTTGAT TATGTTAATA TTAAAATCTA ATAATAAGAT ACTGTAGAAG 50  
5 TATTTTACAT TTTTGGGGTA TAGGCACAAA TATATACATT TAAATATTAG 100  
TAATAGAATT GAACAATTAA CTATAAATA TTATATCATA ATAAACTGTT 150  
GTTTTATCCC AAGGGTAGAG GGA CTCTAAG TAAAACTGTA ACAGAATCAA 200  
10 AAGGTTACTG ATAGTTAGAA TGGGTTGAGA ACTATTTTAA CTTGGGAACT 250  
TTAAATAAGT AAATCT 266

15 (2) INFORMATION FOR SEQ ID :935:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs  
(B) TYPE: nucleic acid  
20 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID :935:

GGAAAACAAA TGTAAGGAGG GAATTCAAAT ACCTAGTTAA TCTATTAAC 50  
ACTAATAACT CATTAAATAA ATTAATAATA TTAAATGATC TGTGTGTTCC 100  
30 ATGCAAATAA CAGAATGATT TCCACTGAAT AGTCATGATG GTTTAAAATA 150  
TTACTCTAAC ACCAATAACA ACACGTAA 178

35 (2) INFORMATION FOR SEQ ID :936:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 base pairs  
(B) TYPE: nucleic acid  
40 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

474

## (xi) SEQUENCE DESCRIPTION: SEQ ID :936:

5 ACTCAGCTCC GTGCGACCCA CATGGCCCCA GCGGGGGGA CACCAGAGGC 50  
TCCTCCATGA GCAGCAGGAG TGAGCGGAGG AATGTGCCCC ACAGCAACTT 100  
TCCCAGCCAA TGCCACGATG GAGATGACAA CCCAGATCT GGGGANACAG 150  
10 AAACCACTCA GAACGGCACA GGGTAACTGG CCCCAAACGC TGAAAGTTAG 200  
ACTTCACCCG AATTACATTT ACCA 224

## (2) INFORMATION FOR SEQ ID :937:

15

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 270 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
20 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :937:

25

ATTTTTTTTC CCAAGAATCC CCAACTCAAT AAAACCGTGA AACAAATTGCT 50  
GGGGATGGGT AGAGAAAACC CATTATAGT ACTTTTCTGC CTTCTTGTGG 100  
30 TTTTCGGCTT TCGGATCAGG GACTGAAGAT AGAAGGAAAA AAAAAAAAAA 150  
AAAACAAACA CAAAAACATT TCAAAAGAGA AAGGAAAAA CTTTTTCCAA 200  
CCAAACTCC TAAAAAACC AAAACAGAA CAACCAATTA AACCCGACCC 250  
35 GACACAATA CCAATGACTG 270

## (2) INFORMATION FOR SEQ ID :938:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 215 base pairs  
(B) TYPE: nucleic acid



475

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :938:

|    |  |     |
|----|--|-----|
|    | AGCCTTCTCC CTATTCGATA AAGATGGCGA TGGCACCATC ACAACAAAGG | 50  |
| 10 | AACTTGGAAC TGTCATGAGG TCACTGGGTC AGAACCCAAC AGAAGCTGAA | 100 |
|    | TTGCAGGATA TGATCAATGA AGTGAATGCT GACGACAATG GCACCATTGA | 150 |
|    | CTTCACAAA TCTTCAACTA TGATGCCTAG AAAAAAGAAA GATACAGATA  | 200 |
| 15 | CTAGAACTAA AGTCA                                       | 215 |

(2) INFORMATION FOR SEQ ID :939:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :939:

|    |  |     |
|----|--|-----|
| 30 | TGTCGTCCTT AATATTTCTN AGCCTTTTGT CATAGAGGTG GTCGGTTGGA | 50  |
|    | CCTCAAAGCC TCCATCTAAT TTTTTTTGTC TATGTTTCTA TATCTCTCTC | 100 |
|    | TTTTACGCTT CTTTCCCGGA CCGTCCCTC CCTCTACAAT TATATTTACT  | 150 |
| 35 | ACCTTCATGA TTGCTTTTTA TTATTCTTT CACTCATCAT TATTGTTTAT  | 200 |
|    | TTTTTAATTA ACAATTTTTT TCATTATTCT TTTTCTTAAT TTGTAACCCG | 250 |
| 40 | TTTCTAATT TCTCAATTAT TGCGCTTTCT CAACCCCCCT CCTTCCTCAT  | 300 |
|    | TAC  | 303 |

476

## (2) INFORMATION FOR SEQ ID :940:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 330 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :940:

ACACTATTTT CAAAATCCA AATAAAGTG CAGTTCAGA CTTTTAAAA 50  
15 AACACCGTT GACCTGTCTT AGTTGTACAT TCAGAAAATG TAGCCTCGAG 100  
CGTTTGCATG CAACACTGCA TATTTTTTCT AATCAGATTA ATATGAGTTT 150  
TAATGTTTAG CATGAAC TAC AGCTAAGGAT AAAAATTTTA AAGTAGCTTT 200  
20 CATAGTCTAG ATTCCTGGTT TCATAATGCT TTATGTAGTA CATTTCAGTT 250  
TGCTTTGCTT TGTGGAGACT TCGCGTATT TTCTTTTGCT TGTTTGTTTA 300  
25 TCGCCAGGCA GCGCTGTTTC AACTGTGAGA 330

## (2) INFORMATION FOR SEQ ID :941:

## (i) SEQUENCE CHARACTERISTICS:

- 30 (A) LENGTH: 107 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :941:

TTTATTTT CAG ATAATTTTAT GTAAACAAAT TAAGAGTTAT TCATTCAAAT 50  
40 TTTTGGCAGT GTTAATCTGT AAATGATGAC TTGATGTACA GAAATGCAT 100

477

TTTTGCT

107

(2) INFORMATION FOR SEQ ID :942:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 126 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :942:

15 CCACAGCATA CACACCTTGG AAACCAAGAA GACTCTTTGT GTGTGTATGT 50  
GTGCGAGACT GACGCGTCTC TACGCGCTCT ATGGGGGAG ATTTGTTAT 100  
TTCGGCGTTA CACCTCCGGT GTTCTC 126

20

(2) INFORMATION FOR SEQ ID :943:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 155 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :943:

ACTGAACAGC CGCTGGTTCC AGAACAGGCA CAGAAGGCTC CAGCGCTAGA 50  
35 AACAACTGGC ACAGGAATGG TAACAATAGT CTGGCTCAGC CACAACAGGA 100  
GGCTCCGGGA CAGTCACAAC CGAGAGCTTC CAGGACAGTT ACAGTCTGTA 150  
AGCTC 155

40

(2) INFORMATION FOR SEQ ID :944:

478

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :944:

10

CGTGAGGAGC AGGTACCATT TTTAGTAGTC ACACAATTCC ACCTCCTGTT 50

TTTACTACTG GCAACTTCTA CTTGAGAATA ATGTTCTGAA AATGGAGGTG 100

15

GGGGGGGGTT TGGAAGCAAA CACATTGTTGG GTTTTAAACC AATTGTTAGG 150

TTCTTTTAT TTAGGGTTGT GCAGGGAAC GTTGGGAGGT TTCTTTAGGT 200

GGGATGGGG GACTGGGTGT TGGTTTTTGG GGGGTTTTTG GGACGGGTTT 250

20

TATTTTGTCC CTTAACTTGG TTTGTTGGGC AGGTGGG 287

## (2) INFORMATION FOR SEQ ID :945:

25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :945:

35

ATCATTGATC AATGATATGG TTTGGATTAC TGCCCCGCCC AAATCTCTTG 50

TCCAATTATA ATCCCAGCA TTGGAGGAGG GGCCCGGTGG GAGGTGATTG 100

GATCATGGGC ATGGACTTCC CCCTTGCTGT TTTCGTGATA ATGAATTCT 149

40

## (2) INFORMATION FOR SEQ ID :946:

479

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 261 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :946:

10

TTTAAACTGC AAATAGTCGT TACAAAAAGT TTTNNNNNTT CTTTTAAATA 50  
AATTTACACAC AAAGAAAGAG AAATAGAAAG CGACGGTAGT GACCAGCAAG 100  
AGGAATAATA ATTACATTCA TCTTAATGTG TGTGTGCCAG TTCTGTTTAC 150  
ATTAACATTG GAAAACTCCA GACCTGGACA CCAGAACCTC AAATCTGTGA 200  
GTGGAATGTC TTGAGATGGG CACGCTGGAA GTCAAAGGGT TTCTCTTTT 250  
TTTTTTTCCC C 261

20

## (2) INFORMATION FOR SEQ ID :947:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :947:

35

CTTTAGGAAC TGTCAGCATG TTGTTGTTGA AGTGTGGAGT TGTAACCTCG 50  
CGTGGACTAT GGACAGTCAA CAATATGTAC TTAAGAGTTG CACTATTGCA 100  
AAACGGGTGT ATTATCCAGG TACTCGTACA CTATTTTTTT GTACTGCTGG 150  
TCCTGTACCA GAAACATTTT CTTTATTGT TACTTGCTTT TTACACTTTG 200

40

480

TTTAGCCACT TAAAATCTGC TTATGGCACA ATTTGCCTCA AAATCCATTC 250

CAAGTTGTAT ATTT 264

5 (2) INFORMATION FOR SEQ ID :948:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 149 base pairs

(B) TYPE: nucleic acid

10 (C) STRANDEDNESS: double

(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :948:

CCTCGACTTA CCACGGGTGA TCCCAGAATG GACTATCAGC GGTGTTTTGA 50

GCCAGGTTGA TTGAGCACTG GGCTCCAAC TATTGTTAAT GAGAAACGGC 100

20 CCAACTTGGA CCATGACTTT CCCATTGCA GGTCTTAGAA TAATTTTTT 149

(2) INFORMATION FOR SEQ ID :949:

25 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

30 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID :949:

35 CGCTCAGGGT GGAAGTGGCC GGGCGCGTCG AATGTGCCGA GCTGGTGCGA 50

GTGGGCGAGC AGAGCGCCTT GAGGTTGAG CATCTTCTGG ATCCAGCAGA 100

GGCCTCCCAG GAGGGGAGCC AGGTGGCTGA AGGCAAGCAC TTTNNNNAGG 150

40 TTCTAGTCCC CTTTTTAGAT CCTAGGGGAC TGGAGATTG GCACCTTCCC 200

481

CCAAGGCTTG GCCTCGTGCC CTATAGGGTG CCCCCCTCTC TT

242

(2) INFORMATION FOR SEQ ID :950:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 153 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :950:

15 ACTCTGCCTG CACTATAAAA TGAACCAAGG AGGATCCAGT TTGCTGTCTG 50  
CACTGACAGA TTTACAGACA GGAAAACAAA GCCTTACTTA CCAGGAATCC 100  
AAAGTTTATA CATGAAAATT TAAAAAGGGA GTCTATGCAA AGCGGAGTTC 150  
20 AGG 153

(2) INFORMATION FOR SEQ ID :951:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 128 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :951:

35 TCGGGGAGTC TCACTGGGGG GGGGACACCT GTGCAAACGC GTAACGCAGG 50  
TTGTTCTCTAA GCGGAGCTCA GGGAGGATAC AGAAACTCT CCTGTGGTGC 100  
TATGAAATGT GCGGTAAAAA GCATTCTG 128

40

(2) INFORMATION FOR SEQ ID :952:

482

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 213 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :952:

10

GTTGGAAATT TCCCTCAAAT CACCTACCGA TTACCCTTGA TTTCCCTTTG 50

TTTTCAGTTT CTCAAAACGA ATGAAATAGA ATATAGCAGA ATGTTAACCC 100

15 ATATAAAAAT AAAGTG TACC CAAATATTGT AATGTATATT GCTGCTCTTC 150

TTCAAATTAA ATAAGGGTTT AAAACCACTT AATTGGTAAT ACAACATCTC 200

AATTGATACA AAT 213

20

## (2) INFORMATION FOR SEQ ID :953:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :953:

GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTT 50

35 TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT 100

TCATTATTTT TTTTCTCTAC CATCATGTAG GCATACTCAG TGTAGACTAC 150

CACAATCCTG GATACCTCTC TGCTTAGATT TACAATCTCT GCTAAGATTT 200

40

GCCACTGCAG AAAGTGTAGT ATTTTCACTA CATTAT 236



483

## (2) INFORMATION FOR SEQ ID :954:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 217 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :954:

GCAGCAGTTT CTTTGAAAAT TTGGACCAGA AGGTGCATAA CAAGTTGTTC 50  
15 TGCAGAAGTT CTTATCTGAT ATTCTTAGGG AGCTATCCTG CATGTAATCT 100  
TCATTTTTTT TTTCTCTACC ATCATGTGAG GCATACCCAG TGTAGACAAC 150  
CACAATCCTG GAAACCTCTC TGCTTAGATT TACAATCTCT GCAAAGATT 200  
20 GCCACTGCAG AAAGTGT 217

## (2) INFORMATION FOR SEQ ID :955:

25

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :955:

35 AGCAGCGACC GCGCTCACTG GCTTTTGT TCTGCTTGGG CCTTTTCTGT 50  
TCAGTCCATG CTTGAACTAC TCCACCCCT TAAATCCAAC GTAAAAACCA 100  
GTCTTTTCTG TGCTTGTCT CTGTGCGTTA ATGCTTTTTC TTATGCTTGC 150  
40 TTATTGAAAT ACTGTATTTT CATTGTCCCC TGGCCAAAAC ATCTGAGTCG 200

484

TGAAACCATT TTAGATACTC TACTTTCTTA CTGTGTTACG TGGCATTTTA 250  
TGCTTG 256

5 (2) INFORMATION FOR SEQ ID :956:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 194 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :956:

CAAGCAATTG AGAGACTTTT TTCCTGTTAT TTTTCTACCA TTTATTTCTC 50  
ATTTTCATTAT ATTATGGTCA GAGAATATAT TTTGAATGAT TTCATTTATT 100  
20 AATTTTAAATAA AATAACATTA AAAAATTTTT TAAATGTGA ATATACCACA 150  
ATACAGTATA AAGATTGTAC ATTCTGTTTT TGGACAGTTT TCTA 194

25 (2) INFORMATION FOR SEQ ID :957:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 196 base pairs  
(B) TYPE: nucleic acid  
30 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID :957:

ATCTATTTTT CTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA 50  
ATAACCTAAA AAAACATGTT TTCTCCACAC TAATTTTAGG GTGAATTCCT 100  
40 CATTCGCTT TTCAGATCAT GGGGTGAGGG GGATGGTTCC TGTGTGTGAG 150

485

GAACTGAGGA ATCAGATGGA AAACAATGCC TCTGCTCCTT TGAGTA

196

(2) INFORMATION FOR SEQ ID :958:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 105 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID :958:

15

GCGCTCAGCT GGAAGTCCG ATCTATTTTT TCTGGTCTC ATACTCAGTT

50

TTTTTATGTA GTCAGTCTAGT AAAATAAACC TAAAAAATAA CATTGATTTT

100

TTCTG

105

20

(2) INFORMATION FOR SEQ ID :959:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 261 base pairs

25

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

30

(xi) SEQUENCE DESCRIPTION: SEQ ID :959:

GACAGCGACC GACACTCAAT GGAATCCCGA TTCCATGGAA ATGGAAAATA

50

35

GCTCTATTTA TACAGCAAAT TCAAATACAG TAGCTTGCTA AGCAACTTCA

100

TAATTCATTA ACACTCGATG GCAGAGCAGA TAGTCACAAT TACTAACGAT

150

TATCATGATC TGCATTCTTG ACAAGTATAC TATGGCGAGA TAAATCAAAC

200

40

TCAGACGATG ATAAGCAAAC TCAAAAATGA AAATGATGAT GCCAACTAAG

250

486

CTTTTGTTAA A

261

## (2) INFORMATION FOR SEQ ID :960:

- 5 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 188 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :960:

15 CACAGTTTGTG TTGACTAAAC TCTACAGAAG TCAGGTATTG GGAAGGAGAA 50  
TCGTTTCTTC TTTAGAGGAG TAGGTTTAA CCATGTTAAA TTTCCAAGAA 100  
TAAATTTATT TATCACCTCT ACACAGCGCA GACCATTTC A GGAAAATAAA 150  
20 TAATTTTCGA TTCAAGTACT ATACAAACTT AACGATGG 188

## (2) INFORMATION FOR SEQ ID :961:

- 25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 191 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :961:

35 ACTTTCGCCT ACCCGGAGAG GCCCAGAAAA TTGACCAGAT GATGGAGGCC 50  
TTCACCCAGC AATACTGCCT ATGCAACCCT GGAGCTTTTC AATCCACAGA 100  
CACACGCTAT GCACTGTCCT TCGCCATCAT AACGCTCAAC ACCAATTCT 150  
40 ACAACCAAAA AGCCAGAGAC AAACCTGACC TAAAGCGCTC C 191

487

## (2) INFORMATION FOR SEQ ID :962:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 191 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :962:

CCAAGGCAGA GTTATTAGG TTTATGCTTT ATATTTATAT ATAAGGTTTT 50  
ATTCATGTTA AAAACTTAAA ACCAACGGAT TATGCAAAGT GATAAGTGTA 100  
TCAATGAATA TACAACTGAC TGGATTTTAA ATATACACAA ACCAGTATAC 150  
CCCCAGTACT TAAATGAAGG CACTCAGTAT ACACCAAAAT T 191

20

## (2) INFORMATION FOR SEQ ID :963:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 178 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :963:

AGCAGGCCAA AAGCCCAGGT GAGGCCAGC AGGAACAGCA GCCCAATGCC 50  
TCCTAGCACT CAAGATCCAC CATAGTCCAA GCAACTGCAG TTACACTTGA 100  
GTACAAATAC GCTCCCGACA GCCTCATGCA GCGACACCCT AAAGGACACC 150  
CGAACACCAT CAATAACCGA ATAGACTA 178

40

## (2) INFORMATION FOR SEQ ID :964:

488

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 199 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :964:

10

ACTTTGCAGT CCTCACATCA CAAATAGAGT AAAAGATTCC CAAAAGGAAG 50

GGGATCCTTT TGA CTGCCAG ACGCGGAAG GAAAGAATGA AATTAAAGAA 100

15

TATCCTTTTA AACACACACC TCGACACAAT TTTCCACTCT GCTAAGGGAT 150

CACAAAGACT AAGACGCGGG CAGACTCCCC ATAAGCCACG CTTATAACC 199

## (2) INFORMATION FOR SEQ ID :965:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :965:

30

ATGGAGCAGG ACCTGCGATG TTCTGATGGA TTATACCCAC AGTGTATTTT 50

GGCACATCTG CCAAAGCTA CAAACAACCC CTAATAATTA CACACTACAG 100

35

ATAGTGAGAA GCGTCCTACC CAGGAGTCCT GAATGTGATC TGAGTATGCT 150

CTAAGGCAGC CCCAGGAAAA GCAATCCAAT CCCTTTCTCC TCGCCTTTAA 200

ACCTGCAGGT TGGGGCT 217

40

## (2) INFORMATION FOR SEQ ID :966:

489

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :966:

10

ATTGCGACC AAAATCATCT GGGTTTATAT TTGAAAAAAC CTTGTTTTCC 50  
AATTTAAAA TGCCAAGAAA GTTGTGAATA CCGTTCATTA TCACTAGGAT 100  
CAAGAAAAAG CAAATGGTTT AACTTTTTAC ATAGGAAATC TAAGAACTAC 150  
TCATCAATAA AACGCAACAC TATCA 175

## (2) INFORMATION FOR SEQ ID :967:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :967:

30

AGGGGTTTCAG GCCTGGAGTC AGGGAAGAAG GGGAAAGGG CAGATAGCTG 50  
GGGGACAAGG AAAACCTGGC GCGAAAAACA CA 92

35

## (2) INFORMATION FOR SEQ ID :968:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 208 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

40

490

## (xi) SEQUENCE DESCRIPTION: SEQ ID :968:

5           GTAATATTAG GGACATGAAT GTTAGTACAG TAATTACCAC ACATGGAAAA           50  
          TATTGTTTCTAG CAGGAAAAGT AAAACTTTCA AAAAATTCCC TAAAGATCCT           100  
          ATTCAATAAA CAATTTTAGA TTTAAGGAAC CACTTACGCA AAACCTCGAAC           150  
10          AAATAACCGA AAACCTCCACC TACCGCGCAA TACTCAAAAA CACAAAAATA           200  
          CTACTAAC   208

## (2) INFORMATION FOR SEQ ID :969:

15

## (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 256 base pairs  
          (B) TYPE: nucleic acid  
          (C) STRANDEDNESS: double  
20          (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID :969:

25

          AGTGGTTGGT GTTTACTGGA ATCTTGTTTT TTTTTTTTCG GTTTTTTTGA           50  
          CTACTCGGGG GGTTTTCCTT TTTTACAGGA ACTAAATCAA CAAACTTTTT           100  
30          CGATTCCTCA ACTTTAGATT TTTATTTTTT TTGATTACCA TTTACTTTTC           150  
          TTCATTTAAA ACTTTTAACG CCTCAGCCTT TTTCTTAGGC CAAGGCCTTC           200  
          CACCAAGGAT TTAATCCGGG ACGGATCTAA CTGGATTTTC CGAGGTGGGT           250  
35          TTAAGA   256

## (2) INFORMATION FOR SEQ ID :970:

40

## (i) SEQUENCE CHARACTERISTICS:

          (A) LENGTH: 240 base pairs  
          (B) TYPE: nucleic acid



491

(C) STRANDEDNESS: double

(D) TOPOLOGY: lin ar

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :970:

AATCTATTTT CCTTGGTCTC ATACTAAGTT TTTTATGTAG TCACTTAGTA 50

10 AATAACCTAA CCCGCTTGTT TTTTCCACAC TAATACTAGG GCGAATTCCT 100

CATTTTATTT TTAAGATCAT GGGGCGAGGG AGATGATCGC GAGCACCAGG 150

ACCTAAGACA TCAGATGAAA AACAAATGCCT CTATTCCTTC AAGTATAATA 200

15

AATGATACCC GAGAGTAAAG AGCTACACTT CGCACCTCTA 240

(2) INFORMATION FOR SEQ ID :971:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :971:

30 ATCTATTTT CTTGGTCTCA TACTCAGTTT TTTATGTAGT CACTTAGTAA 50

ATAACCTAAT CCGCTTGTTT TCTCCACACT AATCCGAGGG TGAATTCCTA 100

ATCTAGCTTT TCAGATCATG GGACGAGGGA AATGACCGCG TCGCGAGGC 150

35

CCTAAGGAAT AACATAGAAA ACACCGCCTC TGCT 184

(2) INFORMATION FOR SEQ ID :972:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 234 base pairs

(B) TYPE: nucleic acid

492

- (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

5

## (xi) SEQUENCE DESCRIPTION: SEQ ID :972:

|  |     |
|--|-----|
| GTGTTCTCTA AGGTGATACC TTTTAATTTT GAAAGACTAA ATAATTTTAA | 50  |
| TCGAGAATTT CCAGTCTTTC AGTCTGATCT ATTAAATTCA CTACTTGTTA | 100 |
| CATAATCCAG TGAAACTCT ACTTGTGAA ATTATGACAT AAAGATCTTG   | 150 |
| CAGCTTTATT TGAGTATTG TTCTTTGTG TAGTTTCCAT CTTTAAAT     | 200 |
| ATTTAAATA TTTCAAGGA TAAAGTATT ATCT                     | 234 |

15

## (2) INFORMATION FOR SEQ ID :973:

20

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

25

## (xi) SEQUENCE DESCRIPTION: SEQ ID :973:

|  |     |
|--|-----|
| TTTTCATCTA AAGGAGAGAG GCAGGCTCAG CTCCTGAAGG TCGCAGAGCC | 50  |
| TCAGTAGTCC TCCTGACTGC GTCTAACTAA CTACCATCAA AAAACAAACA | 100 |
| AAAAAACAT CACAAACTG AACTGCCGCC ATCACCATA CACCAAGTAT    | 150 |
| GTGATTGAAT TATTCAATGA TCTGTTTTCG CGGTAGTGAC CAACANC    | 197 |

35

## (2) INFORMATION FOR SEQ ID :974:

40

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 base pairs  
(B) TYPE: nucleic acid

493

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

5

(xi) SEQUENCE DESCRIPTION: SEQ ID :974:

|    |  |     |
|----|--|-----|
|    | AGCAGGAGAT TTTTTTAATA ATAAACANCA ATGGAGAGGT GGAAATAGAG | 50  |
| 10 | ATGGAAAAAC AGGATCAAAG GAGCAACATA TCCAGTGA CT TAAAAAATA | 100 |
|    | ATCACACGTG GCAAGAAGTT TTCTAAAGTA AACTGTATGT GGGGAGAAGC | 150 |
|    | ATACAGAAAA AAACGAAATA CATAACCCCC CAGGTTTGAA AGAAAATAAT | 200 |
| 15 | TTTGAGTTGT ATCAATCTAT CGATATCAAA GAATGAATGA CCGC       | 244 |

(2) INFORMATION FOR SEQ ID :975:

20

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 330 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID :975:

|    |   |     |
|----|---|-----|
| 30 | TTTTTTTTTC TGAACACTTT GCTTCACACC TTCTCATATT CACGGTTATG  | 50  |
|    | AATTCTCCTG ACTATATCTA TTGTAACCCA AAACAGCAGA CTGTATTTAG  | 100 |
|    | AGACCCATTA GAGATTTTCAT GTCTATATGC CCAGAGCCTG ATATAATGCC | 150 |
| 35 | ACCTTACTAT ACACATAATA TAGAATCTGA GGACTACGTT AACTGATACA  | 200 |
|    | TGTTAAGTAT CCTGCAGAGA GCTGGCACAT TGAATGTGCT CAATAATCGT  | 250 |
| 40 | TAGCTTTAAG TATCTACCTC AAAGGGCTAC TGTGTGACTC CAATGAGATA  | 300 |
|    | ATGTGCAATG AAGGGTTTCG TGTAATATTG                        | 330 |

494

## (2) INFORMATION FOR SEQ ID :976:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 200 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :976:

TGGTGAAAGG AATAAGCAAC TCAAGGTAAA TAAAGAAGAA AGATGAAGAT 50  
15 TCTTAGAATC GTAGAAAGAC TGCAGGGGGA AATAATTAAA GCAGCTTTAT 100  
TCCTTACGGC ATTCATCATT CGTCGAGCTG GAAAGCACTG ACAACTTTGT 150  
AATGAGTTTT TTGCGCTTAA CTCTGTCAGG TGATTATAT GAATNACTTA 200

20

## (2) INFORMATION FOR SEQ ID :977:

## (i) SEQUENCE CHARACTERISTICS:

- 25 (A) LENGTH: 296 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

30

## (xi) SEQUENCE DESCRIPTION: SEQ ID :977:

AAAGGACAAT TTAATATAAA TCTATGTTTG TGCATTTCTG ACAGGCCATT 50  
35 ATTATCTGCT TTGACAAAGC CTTTCTGAAA CGCAGTGTAC AATGAATCTT 100  
AATGATGTTA TGAAACGAGC TTTGCT 3 GCTCTTGATT GGAGCTCCG 150  
GTATGTGATG ACGGTATGTC ATGTATGCAT GGATGTAC 3 AACTGTGTTT 200  
40 AATACTCTGA ATTTAATTA GAAAAAATA CAATAGCAGC AAGGCCCTGG 250

495

TTTCTAAGCT GCATACTTTT ACTAACGCGG GACATGAGCA AATGCC

296

## (2) INFORMATION FOR SEQ ID :978:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 228 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :978:

15

GAATCNCGCC TGACACATAG AATGCATAAA CGAGGGGGGT CCTTCTGCAG

50

ATACTCTAAT CACTACACAG CTTTCTCTAT AAAACTACCC ATAAGCCTTT

100

AACCTTTAGA GAAAAATGAA AAAGGTTAAT GCTTGGAAGC CGGGGGAGGA

150

20

CTGACCACTT CATAAGCCAG TAGGTCTGAG CTGAGTATGC CCCCAGAATC

200

CAGCCACTAC TGATAATTCA CAACGGTA

228

25

## (2) INFORMATION FOR SEQ ID :979:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :979:

CGTACAAAAG CGCTTTGGAG ATGCCAGAAA AAACCCTACG GGAGGGTTAT

50

CCCCCTGACG CTAGGCCATG ACACAATAA ACTTCAATAC ACCAGGACTA

100

40

AGGCAAGTAT GAAGAAGCAA AATATCGTAA CGACGCACCC TCGAGATCTA

150

496

CCAGGCAAAA CCAGAACCTG A

171

## (2) INFORMATION FOR SEQ ID :980:

5

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 241 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

10

## (xi) SEQUENCE DESCRIPTION: SEQ ID :980:

15

TGATTCCCCA TTTCCCTGGA CAGGGCAGAG TCAAGCCGAG AAGGAGGAGC

50

CACAGGCCAG CTGTTAATGA GACACTAAAT AAAACGTTCA GTATTCATAC

100

CTGTGGAACA TGGGTGAACC TTTCTGGTAA CTCGATTTTT CACACCAATG

150

20

ACAGCAAATG AGAAAGTGAG AGAAGCTAGA TAAATGTTTT TAAAGCATTG

200

CTGCAGTGGA AAATAACTGC ACTCTCAGGA CACAGCACTG T

241

25

## (2) INFORMATION FOR SEQ ID :981:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 227 base pairs

(B) TYPE: nucleic acid

30

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :981:

TCACTGCAAT CACGGTAGCT TCGCCCATG CCTCTTCAAC CAGGCACATA

50

CATCGAGAAG TTGAACCTGC ACTTTATTTT ACACTGAACA GACTTACCCC

100

40

GACAACAACA CCTCCCCAGT GGGACAAACC TACCCACCT CCCCACTC

150

497

TACTCCCAGC TAACGTTCCC TATAATCATC ATGACCCATT AACATTTC 200  
AAAACCCACAC TTCAACCCAC AGGAAGA 227

5 (2) INFORMATION FOR SEQ ID :982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs  
(B) TYPE: nucleic acid  
10 (C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID :982:

CGTTGTCGCC ATGGTAATAC CGCTCAGTAC GGGAGGACCC ACAGGCTAAG 50  
ACACTCGGAG CACGAGCTCG CCTGAGGGAC CAACGAGGCG AAGCCACAAT 100  
20 CCGCGAACTC ATGACTGACC CCTTCTAAGT AAGAATCCCA CCCAGGCAAA 150  
CCAATCCGAC AACC GAAATA GCGCAGGCAC CGCCAAATTC AAGGCGCCCC 200  
25 AAAAG 205

(2) INFORMATION FOR SEQ ID :983:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 base pairs  
30 (B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

(xi) SEQUENCE DESCRIPTION: SEQ ID :983:

AGCAACCGGC ACTCAAGTGG AATCCCGAAA AAGTGATTTA AAAATGATCT 50  
40 TACCTGTACC AGAAAAGCAA AATTAAAGGA AACAAAATAA GAACCATAGT 100

498

CCCCAATGAC ATTTAACCGT ACATACAGCG ATAACATGTT CAAAATCCAA 150  
CAAATAACGC AACTTCCAGA CGTAAATATC CGCCACTCGA TTCCCTCCCC 200  
5 CCCT 204

## (2) INFORMATION FOR SEQ ID :984:

(i) SEQUENCE CHARACTERISTICS:  
10 (A) LENGTH: 168 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

15

## (xi) SEQUENCE DESCRIPTION: SEQ ID:984:

ATTGTATTA GAAAAGTAAA GTTGAAGGAA ATAAAATTG CATTCTTGTT 50  
20 TTAAGTGATC TTTAATTGTA TATATCGCGG TAGTATGTTC AAAATCCACT 100  
AAGTACTGTG ACTTTTAGCT GCAAATCTTT GCTCTTTGCT TTTTTTTTTC 150  
25 TTTCTCCCCC CTCCCCAG 168

## (2) INFORMATION FOR SEQ ID :985:

(i) SEQUENCE CHARACTERISTICS:  
30 (A) LENGTH: 350 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: double  
(D) TOPOLOGY: linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID :985:

CTCAGCTGGA ATGTCCGGTG CCTGCTAGGT GCATGGCCAG AGAAGCATGG 50  
40 GCTGGGCCTG GGCACAGGAG GAGCAGCTGC TTTGGTCGGG GTGGAGACTT 100